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120486

From: Vogel, Nancy
Sent: Tuesday, April 27, 2004 1:06 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/677,471

Please search SEQ ID NO 83 of 10/677,471 and return results to me on paper asap.

Thanks,

Examiner Nancy Vogel

Art Unit 1636
Office: Remson 2A65
Mail Box: Remson 2C70
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Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2004, 12:53:47 ; Search time 59 Seconds
(without alignments)
2054.033 Million cell updates/sec

Title: US-10-677-471-83
Perfect score: 2211
Sequence: 1 MFPGGSGSLTYTLVICFLT.....LRRKRSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	431	2	AAV17834
2	2211	100.0	431	3	ABR33428
3	2211	100.0	431	3	ABR33428
4	2211	100.0	431	3	ABR33428
5	2211	100.0	431	4	ABR33428
6	2211	100.0	431	4	ABR33428
7	2211	100.0	431	4	ABR33428
8	2211	100.0	431	4	ABR33428
9	2211	100.0	431	4	ABR33428
10	2211	100.0	431	4	ABR33428
11	2211	100.0	431	4	ABR33428
12	2211	100.0	431	4	ABR33428
13	2211	100.0	431	4	ABR33428
14	2211	100.0	431	4	ABR33428
15	2211	100.0	431	4	ABR33428
16	2211	100.0	431	4	ABR33428
17	2211	100.0	431	4	ABR33428
18	2211	100.0	431	4	ABR33428
19	2211	100.0	431	4	ABR33428
20	2211	100.0	431	4	ABR33428
21	2211	100.0	431	4	ABR33428
22	2211	100.0	431	4	ABR33428
23	2211	100.0	431	4	ABR33428
24	2211	100.0	431	4	ABR33428
25	2211	100.0	431	4	ABR33428

26	2211	100.0	431	6	ABU10960
27	2211	100.0	431	6	ABU11316
28	2211	100.0	431	6	ABU17135
29	2211	100.0	431	6	ABU81712
30	2211	100.0	431	6	ABU86651
31	2211	100.0	431	6	ABU86651
32	2211	100.0	431	6	ADA38026
33	2211	100.0	431	6	ADA21712
34	2211	100.0	431	6	ADA10499
35	2211	100.0	431	6	ADA18043
36	2211	100.0	431	6	ADA28151
37	2211	100.0	431	6	ADA94731
38	2211	100.0	431	6	ADA38956
39	2211	100.0	431	6	ADA93077
40	2211	100.0	431	6	ADA53251
41	2211	100.0	431	7	ADA22638
42	2211	100.0	431	7	ADA22621
43	2211	100.0	431	7	ADA06804
44	2211	100.0	431	7	ADA39497
45	2211	100.0	431	7	ADB96523

ALIGNMENTS

RESULT 1	
AAV17834	AAV17834 standard; protein; 431 AA.
XX	
AC	AAV17834;
XX	
DT	12-AUG-1999 (first entry)
XX	
DE	Human PRO361 protein sequence.
XX	
KW	Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
XX	secreted protein; transmembrane protein; inflammation disorder.
OS	Homo sapiens.
XX	
PN	WO9928462-A2.
XX	
PD	10-JUN-1999.
XX	
PF	01-DEC-1998; 98WO-US025108.
XX	
PR	03-DEC-1997; 97US-0067411P.
XX	
PR	11-DEC-1997; 97US-0069278P.
XX	
PR	11-DEC-1997; 97US-0069334P.
XX	
PR	12-DEC-1997; 97US-0069335P.
XX	
PR	16-DEC-1997; 97US-0069425P.
XX	
PR	16-DEC-1997; 97US-0069694P.
XX	
PR	16-DEC-1997; 97US-0069702P.
XX	
PR	17-DEC-1997; 97US-0069870P.
XX	
PR	17-DEC-1997; 97US-0069873P.
XX	
PR	18-DEC-1997; 97US-0068017P.
XX	
PR	05-JAN-1998; 98US-0070440P.
XX	
PR	09-FEB-1998; 98US-0074086P.
XX	
PR	09-FEB-1998; 98US-0074092P.
XX	
PR	25-FEB-1998; 98US-0075945P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Wood WT, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
XX	
DR	WPI; 1999-371118/31.
XX	
DR	N-PSDB; AAX80059.
XX	
PT	Nucleic acids encoding PRO secreted and transmembrane proteins.
XX	
PS	Claim 12; Fig 37; 123pp; English.
XX	

CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes and
 CC primers. They can be used in a range of diseases related to proteins that
 CC they have homology with, e.g. a PRO protein having homology to complement
 CC proteins may be used in inflammatory responses

CC Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 2; Length 431;

Best Local Similarity 100.0%; Pred. No. 3,6e-173;

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MFFGEGSLTYTLVLIICFTLLRLSASQNLKKSLEDDVVDIQQSSKGRGNEPYTSTQ 60
DB 1 MFFGEGSLTYTLVLIICFTLLRLSASQNLKKSLEDDVVDIQQSSKGRGNEPYTSTQ 60
OY 61 EDCINSCSTKNIISGDKACNLMIFDTRKTARQPCYLFPCPNEBACPDKPAKGLMSYRII 120
DB 61 EDCINSCSTKNIISGDKACNLMIFDTRKTARQPCYLFPCPNEBACPDKPAKGLMSYRII 120
OY 121 TDFPSLTRLNLPQELPQEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTISQKFGSSD 180
DB 121 TDFPSLTRLNLPQELPQEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTISQKFGSSD 180
OY 121 TDFPSLTRLNLPQELPQEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTISQKFGSSD 180
DB 121 TDFPSLTRLNLPQELPQEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTISQKFGSSD 180
OY 181 HLEKLFKMDKDEASQALLAYEKSHSOSQPSDQEIHAHLPEVVSALPATVAVASHTTSA 240
DB 181 HLEKLFKMDKDEASQALLAYEKSHSOSQPSDQEIHAHLPEVVSALPATVAVASHTTSA 240
OY 241 TEKPAITLPTNASVTPSGTSQOPALTTAPPTVTTSQEPPTLLISTVFTRAAATLQAMATT 300
DB 241 TEKPAITLPTNASVTPSGTSQOPALTTAPPTVTTSQEPPTLLISTVFTRAAATLQAMATT 300
OY 301 AVLTTTPQAPTKSGSLPTPTETISNLTNGNYNPNFALSMNVESVTMKTASWEGR 360
DB 301 AVLTTTPQAPTKSGSLPTPTETISNLTNGNYNPNFALSMNVESVTMKTASWEGR 360
OY 361 EASPSSSQSGVPEKNOYGLPFKMLLIGSLFGVLFLVGLVLLRILISESLRRKRYSL 420
DB 361 EASPSSSQSGVPEKNOYGLPFKMLLIGSLFGVLFLVGLVLLRILISESLRRKRYSL 420
OY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

```

RESULT 2

AAB33428 AAB33428 standard; protein; 431 AA.

AC AAB33428;

DT 29-JAN-2001 (first entry)

DE Human PRO361 protein UNQ316 SEQ ID NO:72.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 XX dermatological; antirheritic; antirheumatic; immunosuppressive;
 XX haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 XX antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 XX osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 XX autoimmune thrombocytopenia; immune-mediated renal disease;
 XX demyelinating disease; hepatobiliary disease; Wipple's disease;
 XX inflammatory bowel disease; gluten-sensitive enteropathy;
 XX autoimmune disease; immune-mediated skin disease; allergic disease;
 XX immunological disease; transplantation associated disease;
 XX graft rejection; graft-versus-host-disease.

OS Homo sapiens.

XX MO200053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000MO-US005841.

XX 08-MAR-1999; 99MO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0128849P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99MO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99MO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 08-SEP-1999; 99MO-US020594.
 PR 13-SEP-1999; 99MO-US020944.
 PR 15-SEP-1999; 99MO-US021090.
 PR 15-SEP-1999; 99MO-US021547.
 PR 05-OCT-1999; 99MO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99MO-US028214.
 PR 30-NOV-1999; 99MO-US028313.
 PR 30-NOV-1999; 99MO-US028409.
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 02-DEC-1999; 99MO-US028551.
 PR 02-DEC-1999; 99MO-US028554.
 PR 02-DEC-1999; 99MO-US028565.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030099.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tunes D, Watanabe CK, Wood WI, Yan W;
 XX WPI; 2000-572271/53.
 DR N-PSDB; AAC58593.

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

PS Claim 33; Fig 30; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC selecting and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and

peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58357 to AAC58578 represent PCR primers and hybridization probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB34414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

XX Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 3; Length 431;

Best Local Similarity 100.0%; Pred. No. 3.6e-173;

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MFGGEGSLTYTLVLIICFLTLRLSASQNCCKSLSDVDVIDIOSLSKGRGNEPYTSTQ 60
DB 1 MFGGEGSLTYTLVLIICFLTLRLSASQNCCKSLSDVDVIDIOSLSKGRGNEPYTSTQ 60
QY 61 EDCINSCSTKNISGDKACNLMIFDRTKARQPCNCFPCPNEACPLKPAKGLMSYRII 120
DB 61 EDCINSCSTKNISGDKACNLMIFDRTKARQPCNCFPCPNEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTLRLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
DB 121 TDFPSLTLRLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
QY 121 TDFPSLTLRLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
DB 121 TDFPSLTLRLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
QY 181 HLEKLFKMDASAOQLLAYKEKHSQSQSSDOEIAHLLENVSALPATVAASPHTTSA 240
DB 181 HLEKLFKMDASAOQLLAYKEKHSQSQSSDOEIAHLLENVSALPATVAASPHTTSA 240
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DB 241 TPKEPTLPTNASVPPSGTSQPLATTAPVTVTVTSQPTTISYFTAAATLQAMAT 300
QY 301 AVLTTTFOAPTDSKSLFTIPTETISNLTNGVYNPALSMNSVESSTNMKTASMEGR 360
DB 301 AVLTTTFOAPTDSKSLFTIPTETISNLTNGVYNPALSMNSVESSTNMKTASMEGR 360
QY 361 EASPSGSSQGVENQYGLPFEKMLLIGSLFGLVFLVIGLVLAGRIIISLSRRKRSRL 420
DB 361 EASPSGSSQGVENQYGLPFEKMLLIGSLFGLVFLVIGLVLAGRIIISLSRRKRSRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

```

RESULT 3

AAB01325 standard; protein; 431 AA.

XX AAB01325;

DT 25-SEP-2000 (first entry)

XX Human PRO361 polypeptide.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
 KW PRO715; PRO241; PRO299; PRO233; PRO347; PRO355; PRO353;
 KM PRO361; PRO365; transmembrane polypeptide; antibody; screening;
 XX detection; inhibition; probe; primer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Modified-site 4..10

FT Modified-site 48..54

FT /note= "N-myristoylation site"

FT /note= "N-myristoylation site"

FT Modified-site 50..57
 FT /note= "Tyrosine kinase phosphorylation site"
 FT Modified-site 72..76
 FT /note= "N-glycosylation site"
 FT Modified-site 222..226
 FT /note= "N-glycosylation site"
 FT Modified-site 251..255
 FT /note= "N-glycosylation site"
 FT Modified-site 315..321
 FT /note= "N-myristoylation site"
 FT Modified-site 327..331
 FT /note= "N-glycosylation site"
 FT Modified-site 352..356
 FT /note= "N-glycosylation site"
 FT Domain 384..405
 FT /label= "Transmembrane domain"
 FT Modified-site 415..419
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

XX MO200032776-A2.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 22-DEC-1998; 98US-0113296P.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

XX Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

XX Hillan KJ, Kljavin J, Napier MA, Roy MA, Tumas D, Wood WI;

XX WPI: 2000-412324/35.

XX N-PSDB; AAA49567.

XX New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic agents.

XX Claim 12; Fig 32; 187pp; English.

CC New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described. The membrane-bound CC proteins have various industrial applications, including as CC pharmaceutical and diagnostic agents. The membrane-bound proteins can CC also be employed for screening of potential peptide or small molecule CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO CC antibodies are useful for the affinity purification of PRO from CC recombinant cell culture or natural sources

XX Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 3; Length 431;

Best Local Similarity 100.0%; Pred. No. 3.6e-173;

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MFGGEGSLTYTLVLIICFLTLRLSASQNCCKSLSDVDVIDIOSLSKGRGNEPYTSTQ 60
DB 1 MFGGEGSLTYTLVLIICFLTLRLSASQNCCKSLSDVDVIDIOSLSKGRGNEPYTSTQ 60
QY 61 EDCINSCSTKNISGDKACNLMIFDRTKARQPCNCFPCPNEACPLKPAKGLMSYRII 120
DB 61 EDCINSCSTKNISGDKACNLMIFDRTKARQPCNCFPCPNEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTLRLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
DB 121 TDFPSLTLRLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
QY 181 HLEKLFKMDASAOQLLAYKEKHSQSQSSDOEIAHLLENVSALPATVAASPHTTSA 240

```

Db 101 HLEKLFKMDDEASAOQLAYKEKGHSQSOFSSDOEIAHLLENVSALEPATVAASPHTTSA 240
Qy 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPTTLISTVFTRAAATLOAMATT 300
Db 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPTTLISTVFTRAAATLOAMATT 300
Qy 301 AVLTTTFOAPTDKSGSLETTIPTEISNLTNTGNYNPTALSMNVESSTNNKTRASWGR 360
Db 301 AVLTTTFOAPTDKSGSLETTIPTEISNLTNTGNYNPTALSMNVESSTNNKTRASWGR 360
Qy 361 EASPGSSSGSVPENQYGLPFEKWLILGSLFLGVFLVIGLVLRILISESLRRKRYRSL 420
Db 361 EASPGSSSGSVPENQYGLPFEKWLILGSLFLGVFLVIGLVLRILISESLRRKRYRSL 420
Qy 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431
RESULT 4
AAB34739 ID AAB34739 standard; protein; 431 AA.
AC AAB34739;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human secreted protein encoded by DNA clone vo27 1.
XX
KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO20005375-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007285.
XX
PR 17-MAR-1999; 99US-0124808P.
PR 17-MAR-1999; 99US-0124916P.
PR 17-AUG-1999; 99US-0146339P.
PR 01-OCT-1999; 99US-0157247P.
PR 29-NOV-1999; 99US-0167824P.
PR 15-FEB-2000; 2000US-0182711P.
XX
PA (ALPH-) ALPHAGENE INC.
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-638211/61.
DR N-PSDB; AAC59840.
XX
PT Novel proteins and polypeptides useful for the treatment of e.g multiple
PT sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer,
PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
XX
PS Claim 114; Page 453-455; 493pp; English.
XX
CC This invention relates to 59 human secreted proteins and the nucleotide
CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
CC represent the proteins and their encoding nucleotide sequences, and
CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for
CC the DNA sequences are represented by sequences AAC59847-C59956. The
CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
CC antiinflammatory, antinaeemic, noctropic, antiparkinsonian,
CC cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,

CC antibacterial, virucide, and fungicide activity. The proteins and
CC nucleotide sequences are useful as nutritional sources or supplements and
CC in research. The proteins are useful for treating immune deficiency and
CC disorders, which may be genetic or resulting from infections, autoimmune
CC disorders such as multiple sclerosis, systemic lupus erythematosus,
CC rheumatoid arthritis, and for treating myeloid or lymphoid cell
CC deficiencies such as anaemias by regulating haematopoiesis. The proteins
CC are also useful in compositions for bone, cartilage, tendon, ligament
CC and/or nerve tissue growth or regeneration, for wound healing, tissue
CC repair and replacement and in the treatment of wounds, incisions and
CC ulcers. Other uses include in the treatment of central and peripheral
CC nervous system and neuropathies such as Alzheimer's and Parkinson's
CC diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
CC such as spinal cord disorders, head trauma and stroke. The proteins may
CC also be used as a contraceptive, and for treating coagulation disorders
CC such as haemophilias. The protein and nucleotide sequences with cadherin
CC activity are useful for treating cancer. Other uses for the protein
CC include for inhibiting the growth, infection or function of, or killing,
CC infectious agents such as bacteria, virus, fungi and other parasites, for
CC effecting bodily characteristics such as height, weight, hair colour,
CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,
CC catabolism, anabolism, processing, utilization, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
CC effecting behavioural characteristics, providing anaesthetic effects and
CC for treating hyperproliferative disorders such as psoriasis

XX Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 3; Length 431;

Best Local Similarity 100.0%; Pred. No. 3.6e-173; Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFPGEGSLTFTVLVICTLRLASQNLKSLSEVDVIDIQSSLSKGRGNEPVYTSQ 60
Db 1 MFPGEGSLTFTVLVICTLRLASQNLKSLSEVDVIDIQSSLSKGRGNEPVYTSQ 60
Qy 61 EDCINSCSTKNIISGDKACNLMIFDTRKTAQPCNYLFCPCNEBACPUPKAGLMSYRII 120
Db 61 EDCINSCSTKNIISGDKACNLMIFDTRKTAQPCNYLFCPCNEBACPUPKAGLMSYRII 120
Qy 121 TDFPSLTRNLPSQELPOEDSLIHQFQSAVTPPLAHHTDYSKPDISWRDLSQKFGSSD 180
Db 121 TDFPSLTRNLPSQELPOEDSLIHQFQSAVTPPLAHHTDYSKPDISWRDLSQKFGSSD 180
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Db 181 HLEKLFKMDDEASAOQLAYKEKGHSQSOFSSDOEIAHLLENVSALEPATVAASPHTTSA 240
Qy 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPTTLISTVFTRAAATLOAMATT 300
Db 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPTTLISTVFTRAAATLOAMATT 300
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Db 301 AVLTTTFOAPTDKSGSLETTIPTEISNLTNTGNYNPTALSMNVESSTNNKTRASWGR 360
Qy 361 EASPGSSSGSVPENQYGLPFEKWLILGSLFLGVFLVIGLVLRILISESLRRKRYRSL 420
Db 361 EASPGSSSGSVPENQYGLPFEKWLILGSLFLGVFLVIGLVLRILISESLRRKRYRSL 420
Qy 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431
RESULT 5
AAB35464 ID AAB35464 standard; protein; 431 AA.
XX
AC AAB35464;
XX
DT 26-JUN-2001 (first entry)
XX

DE Human protein sequence SEQ ID NO:17950.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX 27-AUG-1999; 99JP-00300253.
XX 11-JAN-2000; 2000JP-00118776.
XX 02-MAY-2000; 2000JP-00183767.
XX 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Makamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX length CDNA's defined in the specification, and for the detection and/or
XX diagnosis of the abnormality of the proteins encoded by the full-length
XX CDNA's.
XX
XX Claim 8; SEQ ID NO 17950; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX length CDNA's defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in the
XX specification. The primer sets can be used in antisense therapy and in
XX gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length CDNA's. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length CDNA's. The primers allow obtaining of the full-length
XX CDNA's easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human CDNA sequences; AAB92446 to AAB95893
XX represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX oligonucleotides, all of which are used in the exemplification of the
XX present invention
XX
XX Sequence 431 AA:
SQ
Query Match 100.0%; Score 2211; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.6e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFFGGGSLTYTVIICPLTLRLASASONCLKKSLLEVDVIDIOSLSKGRGNPPVTSQ 60
DB 1 MFFGGGSLTYTVIICPLTLRLASASONCLKKSLLEVDVIDIOSLSKGRGNPPVTSQ 60
QY 61 EDCINSCSTKNISGDKACNLMIPTDKTARQPCYLFPCPNBEACPLKPAKGLMSYRII 120
DB 61 EDCINSCSTKNISGDKACNLMIPTDKTARQPCYLFPCPNBEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRNLPSQELPQEDSLHGFQSOAVTPLAHHHTDYSKPTDISISWRDTSLSQKFGSSD 180
DB 121 TDFPSLTRNLPSQELPQEDSLHGFQSOAVTPLAHHHTDYSKPTDISISWRDTSLSQKFGSSD 180

QY 181 HLEKLFKXDEASAOQLLAYKEKGSSQSFSSDQETIAHLPPENVSALPATVAVASPHTTSA 240
DB 181 HLEKLFKXDEASAOQLLAYKEKGSSQSFSSDQETIAHLPPENVSALPATVAVASPHTTSA 240
QY 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPTTWTYSQPTTLISVTFRAAATTOAMATT 300
DB 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPTTWTYSQPTTLISVTFRAAATTOAMATT 300
QY 301 AVLTTPQAPDPSKGSLETIPTEISNLTNTGNVYNPTALSMNSVESSTWAKTASMEGR 360
DB 301 AVLTTPQAPDPSKGSLETIPTEISNLTNTGNVYNPTALSMNSVESSTWAKTASMEGR 360
QY 361 EASPGSSSQSVPENQYGLPEKMLLIGSLFGVLFLVIGLGRILISESLRRRRYSRL 420
DB 361 EASPGSSSQSVPENQYGLPEKMLLIGSLFGVLFLVIGLGRILISESLRRRRYSRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431
RESULT 6
AAB65299
ID AAB65299 standard; protein; 431 AA.
XX
XX AAB65299;
AC 02-APR-2001 (first entry)
XX
XX DT 02-APR-2001 (first entry)
XX
XX DE Human PRO361 protein sequence SEQ ID NO:515.
XX
XX KW Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX
XX OS Homo sapiens.
XX
XX PN WO200073454-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 30-MAR-2000; 2000WO-US008439.
XX
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 07-JUL-1999; 99US-0143048P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 17-AUG-1999; 99US-0149396P.
XX PR 15-SEP-1999; 99WO-US02109P.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 08-OCT-1999; 99US-0158663P.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 22-FEB-2000; 2000WO-US004414.
XX PR 24-FEB-2000; 2000WO-US004914.
XX PR 24-FEB-2000; 2000WO-US005004.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 15-MAR-2000; 2000WO-US006884.
XX PR 20-MAR-2000; 2000WO-US007377.
XX
XX (GENTH) GENENTECH INC.
XX
XX AShtenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferreira N, Fong S, Geider H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
 PI Zhang Z;
 XX WPI; 2001-032160/04.
 DR N-PSDB; AAF44268.
 XX PRO polynucleotides used to produce polypeptides used to target bioactive
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX
 XX Claim 12; Fig 32b; 935bp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 CC
 XX Sequence 431 AA;
 SQ
 Query Match 100.0%; Score 2211; DB 4; Length 431;
 Best Local Similarity 100.0%; Pred. No. 3.6e-173;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFFGGESLVTYLVITICFLTLRLSASQNCCKKSLDVIDIQSSLSKGRNPEVYTSTQ 60
 DB 1 MFFGGESLVTYLVITICFLTLRLSASQNCCKKSLDVIDIQSSLSKGRNPEVYTSTQ 60
 QY 61 EDCINSCSTKNISGDKACNLMIFTRKTAARPNCYLPFCNPEKACPLKPAKGLMSYRII 120
 DB 61 EDCINSCSTKNISGDKACNLMIFTRKTAARPNCYLPFCNPEKACPLKPAKGLMSYRII 120
 QY 121 TDFPSELTNLPQOEIPQEDSLHGFQSOAVTFLAHNHDYSKPTQISMRDTSOKFGSSD 180
 DB 121 TDFPSELTNLPQOEIPQEDSLHGFQSOAVTFLAHNHDYSKPTQISMRDTSOKFGSSD 180
 QY 181 HLEKLFKXDEASAOGLLAYKEKHSQSOFSSDOEIAHLLENVSALEPATVAASPHTTSA 240
 DB 181 HLEKLFKXDEASAOGLLAYKEKHSQSOFSSDOEIAHLLENVSALEPATVAASPHTTSA 240
 QY 241 TPKPATLLPTNASVTPSGTSQOLATTAPRYTTSVSQPTTLISVFRRAATLLOAMATT 300
 DB 241 TPKPATLLPTNASVTPSGTSQOLATTAPRYTTSVSQPTTLISVFRRAATLLOAMATT 300
 QY 301 AVLTTPPAOPTDSKSLLETIPTEISNLTNTGNYNPTLASMSNVESSTMNKTASWEGR 360
 DB 301 AVLTTPPAOPTDSKSLLETIPTEISNLTNTGNYNPTLASMSNVESSTMNKTASWEGR 360
 QY 361 EASPSGSSQSVENQYGLPFEKWLIGSLFGLVFLVIGLVLGRILSESILRRKRYRSL 420
 DB 361 EASPSGSSQSVENQYGLPFEKWLIGSLFGLVFLVIGLVLGRILSESILRRKRYRSL 420
 QY 421 DYLINGIYVDI 431
 DB 421 DYLINGIYVDI 431

XX
 DE Human secreted/transmembrane protein PRO361.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; anti-HIV;
 KW cyostatic; antiarteriosclerotic; antiinflammatory; antidiabetic;
 KW cardiac; AIDS; acquired immunodeficiency syndrome; cancer;
 KW atherosclerosis; inflammatory disease; diabetic complication;
 KW cardiac injury; organ failure.
 XX
 OS Homo sapiens.
 XX
 PN US2002142959-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 31-AUG-2001; 2001US-00944654.
 XX
 PR 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Bocstein D, Baton DL, Ferrara N, Filvaroff E;
 PI Geritken ME, Goddard A, Godowski PJ, Gimaldi JC, Gurney AL;
 PI Hillan KJ, Kijavini IV, Napier MA, Roy MA, Tumas D, Wood WT;
 XX
 DR WPI; 2003-174141/17.
 XX N-PSDB; ABX75504.
 XX
 PT New isolated PRO polypeptide and encoding nucleic acid, useful for the
 PT diagnosis and treatment of disorders associated with the PRO polypeptide,
 PT such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 XX
 PS Claim 12; Fig 32; 178bp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (a secreted or
 CC transmembrane protein) comprising: (a) at least 80% sequence identity or
 CC positives when compared to any of 15 sequences, fully defined in the
 CC specification, lacking or with its associated signal peptide; or (b) at
 CC least 80% sequence identity to a sequence encoded by the full-length
 CC coding sequence of a DNA deposited in the American Type Culture
 CC Collection (ATCC). Also included are: (1) an isolated nucleic acid
 CC comprising: (a) at least 80% sequence identity to a nucleotide sequence
 CC that encodes a PRO protein; (b) at least 80% sequence identity to a
 CC nucleotide sequence or full-length coding sequence with any of 15 fully
 CC defined sequences of 957-1441 base pairs, given in the specification; or
 CC (c) at least 80% sequence identity to a full-length coding sequence of a
 CC DNA deposited under ATCC Accession No. 209526, 209524, 209528,
 CC 209530, 209523, 209532, 209531, 209529, 209527, 209570, 209618,
 CC 209621 or 209619; (2) a vector comprising the nucleic acid; (3) a host
 CC cell comprising the vector which, when cultured under conditions suitable
 CC for expression of the PRO polypeptide, produces the PRO protein; (4) a
 CC chimeric molecule comprising PRO fused to a heterologous amino acid
 CC sequence; and (5) an anti-PRO antibody. The methods and compositions of
 CC the present invention are useful for the diagnosis and treatment of
 CC disorders associated with the PRO polypeptide, such as AIDS (acquired
 CC immunodeficiency syndrome), cancer, atherosclerosis, inflammatory
 CC disease, diabetic complications, cardiac injury and organ failure. The

CC antibodies can also be used in the different screening, therapeutic and
CC biological assays. The present sequence represents a PRO protein
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,6e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGGEGSLTYTLVLIICFLTLRLSASQNLKSLDENVIDIOSLSKIRGNEPYVTSQ 60
DB 1 MFFGGEGSLTYTLVLIICFLTLRLSASQNLKSLDENVIDIOSLSKIRGNEPYVTSQ 60
QY 61 EDCINSCCTKNIISGDKACNLMIPTDKTAROPNCYLCFCPNEBACPLKPAKGLMSYRII 120
DB 61 EDCINSCCTKNIISGDKACNLMIPTDKTAROPNCYLCFCPNEBACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRLNLPQDELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISWBDTLSQKFGSSD 180
DB 121 TDFPSLTRLNLPQDELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISWBDTLSQKFGSSD 180
QY 181 HLEKLPKMDASAOQLAYKEKHSQSSQPSOEIAHLHPENVSAIPATVAASPTTSA 240
DB 181 HLEKLPKMDASAOQLAYKEKHSQSSQPSOEIAHLHPENVSAIPATVAASPTTSA 240
QY 241 TKPKATLPTNASVTPSGTSOPQLATTAPVTVTSQPPPTLISVETRAAATLQMATTT 300
DB 241 TKPKATLPTNASVTPSGTSOPQLATTAPVTVTSQPPPTLISVETRAAATLQMATTT 300
QY 301 AVLTTTFOAPTDKSGSLFTIPTEISNLTANTGNVNPALSMNSVESSTNNKTASWEGR 360
DB 301 AVLTTTFOAPTDKSGSLFTIPTEISNLTANTGNVNPALSMNSVESSTNNKTASWEGR 360
QY 361 EASPSGSSGGSVPENQYGLPFEXMILIGSLFGVLFVLVGLGRIISESLRRKRYSL 420
DB 361 EASPSGSSGGSVPENQYGLPFEXMILIGSLFGVLFVLVGLGRIISESLRRKRYSL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

RESULT 8
ABUS8114
ID ABUS8114 standard; protein; 431 AA.
XX
AC ABUS8114;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #146.
XX
KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADAPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
XX 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 26-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.

PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093333P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095923P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019431.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0144698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0148396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.

PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004314.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,6e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPGSGSLTYTLVILICGLTRLSASONCLKKSLEDVVIDIQSSLSKIGRNEPVYSTQ 60
DB 1 MFPGSGSLTYTLVILICGLTRLSASONCLKKSLEDVVIDIQSSLSKIGRNEPVYSTQ 60
QY 61 EDCINSCCSTKNISGDACNLMIFDTRKTAQPNICYLFFCNEBACPLKPAKGLMSYRII 120
DB 61 EDCINSCCSTKNISGDACNLMIFDTRKTAQPNICYLFFCNEBACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRNLPSQELPOEDSLIHGQFSQAVTPLAHHHTDYSKPFDISWRDTLSQKFGSSD 180
DB 121 TDFPSLTRNLPSQELPOEDSLIHGQFSQAVTPLAHHHTDYSKPFDISWRDTLSQKFGSSD 180
QY 181 HLEKLFKMDASAOULAYKEKGHSQSSQSSDOEIAHLHPNVNAPLPTVAVAPHTTSA 240
DB 181 HLEKLFKMDASAOULAYKEKGHSQSSQSSDOEIAHLHPNVNAPLPTVAVAPHTTSA 240
QY 241 TPKPATLLPTNASVPSGTSQPOLATTAPVTVTSQPTTLISTVFTRAATIQAMATT 300
DB 241 TPKPATLLPTNASVPSGTSQPOLATTAPVTVTSQPTTLISTVFTRAATIQAMATT 300
QY 301 AVLTTTFOAPTDSKGSLETTIPTEISNLTNTGNVNPETALSMNSVBSSTNNKTASWEGR 360
DB 301 AVLTTTFOAPTDSKGSLETTIPTEISNLTNTGNVNPETALSMNSVBSSTNNKTASWEGR 360
QY 361 EASPESSSQSGVPENQYGLPREKWLITGSLLFYULFVLYIGVLLGRILISELRKKRYRRL 420
DB 361 EASPESSSQSGVPENQYGLPREKWLITGSLLFYULFVLYIGVLLGRILISELRKKRYRRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431
RESULT 9
ABUS9192
ID ABUS9192 standard; protein; 431 AA.
AC ABUS9192;
XX 28-APR-2003 (first entry)
DT Novel human secreted or transmembrane protein PRO361.
XX
DE
XX

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disease;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX Homo sapiens.
 OS US2002132252-A1.
 PN 19-SEP-2002.
 XX 14-NOV-2001; 2001US-0090442.
 PF 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US02006S.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 03-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 02-MAR-2000; 2000WO-US005004.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006319.
 PR 20-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001WO-US021992.
 XX (GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gertlsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WT;
 PI Zhang Z;
 DR WPI: 2003-247083/24.
 DR N-PSDB; ABX80473.
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments.
 XX
 PS Claim 12; Fig 328; 648pp; English.
 XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, and PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,

CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO110, PRO844, PRO112, PRO192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
CC
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.6e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGGEGSLTYTLVLTICFTLRSLASQNCLEKSLSDVDVLDIQSLSKGIRGNEPYTSTQ 60
DB 1 MFGGEGSLTYTLVLTICFTLRSLASQNCLEKSLSDVDVLDIQSLSKGIRGNEPYTSTQ 60
QY 61 EDCINSCSTKNISGDKACNLMIFDTRKTARQPNCYLFFECPEAEACPLKPAKGLMSYRII 120
DB 61 EDCINSCSTKNISGDKACNLMIFDTRKTARQPNCYLFFECPEAEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTNLNLPQELPQEDSLHGGFSAVTPLAHHHDYSKPTDISMRDILSQKFGSSD 180
DB 121 TDFPSLTNLNLPQELPQEDSLHGGFSAVTPLAHHHDYSKPTDISMRDILSQKFGSSD 180
QY 121 TDFPSLTNLNLPQELPQEDSLHGGFSAVTPLAHHHDYSKPTDISMRDILSQKFGSSD 180
DB 121 TDFPSLTNLNLPQELPQEDSLHGGFSAVTPLAHHHDYSKPTDISMRDILSQKFGSSD 180
QY 181 HLEKLPKMDKDEASQALAAVEKSHSOSQSSDOETIAHLPEVNSALPATVAVASHTTSA 240
DB 181 HLEKLPKMDKDEASQALAAVEKSHSOSQSSDOETIAHLPEVNSALPATVAVASHTTSA 240
QY 241 TPKPATLLPTNASVTPSGTSPQALATTAPVTVTTSQPTTLISVFTFRAAATLQAMATT 300
DB 241 TPKPATLLPTNASVTPSGTSPQALATTAPVTVTTSQPTTLISVFTFRAAATLQAMATT 300
QY 301 AVLTTFQAPPTSKSLFTPTETISNLTNGVYNNPPLASMSNVESSTNMKTSWGR 360
DB 301 AVLTTFQAPPTSKSLFTPTETISNLTNGVYNNPPLASMSNVESSTNMKTSWGR 360
QY 361 EASPPSSQSGVPENOYGLPFEKMLLIGSLFGLVFLVIGVLGRILSESIRKRYRSL 420
DB 361 EASPPSSQSGVPENOYGLPFEKMLLIGSLFGLVFLVIGVLGRILSESIRKRYRSL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

RESULT 10

ABU82704
ID ABU82704 standard; protein; 431 AA.
AC ABU82704;
DT 26-JUN-2003 (first entry)
DE Human secreted/transmembrane protein PRO361.
XX
XX Human; PRO: secreted protein; transmembrane protein;
KM cardiac insufficiency disorders; angiogenesis; wound healing;
KM cancerous tumour; immune response; retinal disorder; sight loss;
KM retinitis pigmentosa; age-related macular degeneration; AMD;
KM kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KM Crohn's disease; sports injury; arthritis.
OS Homo sapiens.
XX

PN US2003032023-A1.
PD 13-FEB-2003.
XX 14-NOV-2001; 2001US-00990711.
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088023P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
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XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089533P.
XX 17-JUN-1998; 98US-0089538P.
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XX 17-JUN-1998; 98US-0089599P.
XX 17-JUN-1998; 98US-0089600P.
XX 17-JUN-1998; 98US-0089653P.
XX 18-JUN-1998; 98US-0089801P.
XX 18-JUN-1998; 98US-0089807P.
XX 18-JUN-1998; 98US-0089908P.
XX 19-JUN-1998; 98US-0089947P.
XX 19-JUN-1998; 98US-0089948P.
XX 19-JUN-1998; 98US-0089952P.
XX 22-JUN-1998; 98US-0090246P.
XX 22-JUN-1998; 98US-0090252P.
XX 22-JUN-1998; 98US-0090254P.
XX 23-JUN-1998; 98US-0090349P.
XX 23-JUN-1998; 98US-0090355P.
XX 24-JUN-1998; 98US-0090429P.
XX 24-JUN-1998; 98US-0090431P.
XX 24-JUN-1998; 98US-0090435P.
XX 24-JUN-1998; 98US-0090444P.
XX 24-JUN-1998; 98US-0090445P.
XX 24-JUN-1998; 98US-0090472P.
XX 24-JUN-1998; 98US-0090535P.
XX 24-JUN-1998; 98US-0090540P.
XX 24-JUN-1998; 98US-0090542P.

[illegible]

PR	08-MAR-1999;	99WO-US005028.
PR	12-MAR-1999;	99US-01239572.
PR	02-JUN-1999;	99WO-US012252.
PR	23-JUN-1999;	99US-0141037P.
PR	07-JUL-1999;	99US-0143048P.
PR	20-JUL-1999;	99US-0144758P.
PR	26-JUL-1999;	99US-0145698P.
PR	28-JUL-1999;	99US-0146222P.
PR	17-AUG-1999;	99US-0149396P.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	08-OCT-1999;	99US-0158663P.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028301.
PR	01-DEC-1999;	99WO-US028634.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	05-JAN-2000;	2000WO-US0003219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	24-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-2000;	2000WO-US013358.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	23-JUN-2000;	2000US-0213637P.
PR	28-JUL-2000;	2000WO-US020710.
PR	11-AUG-2000;	2000WO-US022031.

Query Match	100.0%	Score 2211	DB 6	Length 431	
Best Local Similarity	100.0%	Prid. No. 3,6e-173			
Matches 431	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	MFPGEGSLYTVLIIICFLTLRLSASONCKKSLSEDVVIDIQSSLKSGIRGNEPVYSTQ	60		
DB	1	MFPGEGSLYTVLIIICFLTLRLSASONCKKSLSEDVVIDIQSSLKSGIRGNEPVYSTQ	60		
QY	61	EDCJNSCCSTKNIISGDYKACNIMIFDTRKTAQPCYLFPCNEEACPLKPAKGLMSYRII	120		
DB	61	EDCJNSCCSTKNIISGDYKACNIMIFDTRKTAQPCYLFPCNEEACPLKPAKGLMSYRII	120		
QY	121	TDPSFLTRNLPSQELPOEDSLIHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD	180		
DB	121	TDPSFLTRNLPSQELPOEDSLIHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD	180		
QY	181	HLEKLPKMDKESAQULLAYKEKGHQSSQSFSSDGEIAHLHPENNVALPATVAVASPHHTSA	240		
DB	181	HLEKLPKMDKESAQULLAYKEKGHQSSQSFSSDGEIAHLHPENNVALPATVAVASPHHTSA	240		
QY	241	TPKRAATLLPNTASVTPSGTSPOLATTAAPPTVYTSOPTLLISTVFRAAATLOAMATT	300		
DB	241	TPKRAATLLPNTASVTPSGTSPOLATTAAPPTVYTSOPTLLISTVFRAAATLOAMATT	300		
QY	301	AVLPTTFQAPDPSKGSLETTIPFTEISMLTLNTGAVNPTLASMNVESSTMNKTASMEGR	360		
DB	301	AVLPTTFQAPDPSKGSLETTIPFTEISMLTLNTGAVNPTLASMNVESSTMNKTASMEGR	360		
QY	361	EASPGSSSQGSVPENQYGLPEPEKULLIGSLLEGVLFVLIGLVLLGRILISESLRRKRYISRL	420		
DB	361	EASPGSSSQGSVPENQYGLPEPEKULLIGSLLEGVLFVLIGLVLLGRILISESLRRKRYISRL	420		
QY	421	DYLLNGIYVDI 431			
DB	421	DYLLNGIYVDI 431			

RESULT 11
ABU60623
ID ABU60623 standard; protein; 431 AA.
XX
AC ABU60623;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #182.
XX
DE Human, PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KM diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992538.
XX
PR 15-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
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PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
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PR 11-JUN-1998; 98US-0088867P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
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PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
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PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089807P.
PR 18-JUN-1998; 98US-0089908P.

PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004314.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023532.
PR 24-AUG-2000; 2000WO-US023338.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941932.
XX
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR N-PDB; ABX90451.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 12; Fig 328; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC segdata.uspto.gov/sequence.html

XX SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,66-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGGESLTYTVIIICFLTLRLSASQNLKKSLEEDVNDIOSLSKGRNEPVYTSTQ 60
Db 1 MFFGGESLTYTVIIICFLTLRLSASQNLKKSLEEDVNDIOSLSKGRNEPVYTSTQ 60
QY 61 EDCINSCSTKNISGDKACNLMIPDTRKTAROPNCYLFCPNEBACPLKPAKGLMSYRII 120
Db 61 EDCINSCSTKNISGDKACNLMIPDTRKTAROPNCYLFCPNEBACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRNLPSQELPQEDSLHGFSAQVTPLAHHHTYSKPTDISWRDTLSOKRGSSD 180
Db 121 TDFPSLTRNLPSQELPQEDSLHGFSAQVTPLAHHHTYSKPTDISWRDTLSOKRGSSD 180
QY 181 HLEKLFKMDASAQQLAYKEKGHSOSSQPSDOEIAHLLENVSALPATVAASPHTTSA 240
Db 181 HLEKLFKMDASAQQLAYKEKGHSOSSQPSDOEIAHLLENVSALPATVAASPHTTSA 240
QY 241 TPKPATLPTNASVTPSGTSGPOLATTAPVTVTSQPTTLISTVFTRAATLQAMATT 300
Db 241 TPKPATLPTNASVTPSGTSGPOLATTAPVTVTSQPTTLISTVFTRAATLQAMATT 300
QY 301 AVLTTFQAPTSKGSLETFIPTEISNLTINGNVNPALMSNVESSTMKTASWEGR 360
Db 301 AVLTTFQAPTSKGSLETFIPTEISNLTINGNVNPALMSNVESSTMKTASWEGR 360
QY 361 EASPGSSSGSVPENQYGLPFEXMLIGSLFGVLVGLVGLGRILSESLRRKRYSTL 420
Db 361 EASPGSSSGSVPENQYGLPFEXMLIGSLFGVLVGLVGLGRILSESLRRKRYSTL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

RESULT 12
ABU14005
ID ABU14005 standard; protein; 431 AA.
XX
AC ABU14005;
XX
DT 26-FEB-2003 (first entry)
XX
DE Human PRO361 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2002103125-A1.
XX
PD 01-AUG-2002.
XX
PF 20-NOV-2001; 2001US-00989731.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0076910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088012P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088325P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089402P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012525.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028310.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GENENTECH LTD.
PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gerner H, Gerlitsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoletti NF,
PI Roy MA, Stewart TA, Tuma D, Watanabe CK, Williams PM, Wood WT,
PI Zhang Z;
XX
XX WPI; 2003-102117/09.
DR N-PSDB; ABX64297.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
XX antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 12; Fig 326; 649pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. ABU1860-
CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/patid/patidentry.html
XX
XX Sequence 431 AA;
SQ
Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,66-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFFGEGSLTYTVLIIICPLTLRLSASQNCCKSLSDVVIDIGSSLSKGRNEPYTSTQ 60
DB 1 MFFGEGSLTYTVLIIICPLTLRLSASQNCCKSLSDVVIDIGSSLSKGRNEPYTSTQ 60
QY 61 EDCINSCSTKNISGDKACNLMIFTRKTAARPNPCYLPFCPEBEACPLKPAKGLMSYKII 120
DB 61 EDCINSCSTKNISGDKACNLMIFTRKTAARPNPCYLPFCPEBEACPLKPAKGLMSYKII 120
QY 121 TDFPSTLTNLPSQELPOEDSLHGFSAVTPDLAHHHTDYSKPTDISNRDITLSQKFGSSD 180
DB 121 TDFPSTLTNLPSQELPOEDSLHGFSAVTPDLAHHHTDYSKPTDISNRDITLSQKFGSSD 180
QY 181 HLEKLFKXDEASQQLLAYKEKHSQSQFSSDOEIAHLHPENVASALPATVAVASPTTSA 240
DB 181 HLEKLFKXDEASQQLLAYKEKHSQSQFSSDOEIAHLHPENVASALPATVAVASPTTSA 240
QY 241 TPKPATLPTNASVTPSGTSQQLATTAAPTPTTTSQPTTTLISTVFTRAAATLQAMATT 300

DB 241 TPKPATLPTNASVTPSGTSQQLATTAAPTPTTTSQPTTTLISTVFTRAAATLQAMATT 300
QY 301 AVLTTFQAPPTDSKSGLETTIFTEISNLTNTGWNVPALSMNSVSESTANKTASMEGR 360
DB 301 AVLTTFQAPPTDSKSGLETTIFTEISNLTNTGWNVPALSMNSVSESTANKTASMEGR 360
QY 361 EASPGSSQGSVPENQYGLPFEKMLIGSLFGVLFLVTGLVLLGRITSESLRRKRSRL 420
DB 361 EASPGSSQGSVPENQYGLPFEKMLIGSLFGVLFLVTGLVLLGRITSESLRRKRSRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431
RESULT 13
ABU60244
ID ABU60244 standard; protein; 431 AA.
XX
XX ABU60244;
AC
XX
XX 24-APR-2003 (first entry)
DT
XX
XX Human PRO polypeptide #15.
DE
XX Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer;
XX inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility;
XX birth defect; premature aging; diabetes; dog; cat; horse;
XX acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit;
XX industry; cytostatic; antiinflammatory; cardiac; antifertility;
XX anti-HIV; antitartaric; antidiabetic.
XX
XX Homo sapiens.
OS
XX US2002132768-A1.
PN
XX 19-SEP-2002.
PD
XX
XX 31-AUG-2001; 2001US-00945015.
PF
XX 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074068P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-00216021.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-0021851P.
PR 22-DEC-1998; 98US-0113296P.
PR 03-MAR-1999; 99US-00254311.
PR 22-JUN-1999; 99US-00514252.
PR 28-JUL-1999; 99US-0146223P.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Boretstein D, Eaton DL, Ferrara N, Filvaroff E,
PI Gerlicsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gunney AL,
PI Hillan KJ, Kijavini J, Napier MA, Roy MA, Tumas D, Wood WI;
XX
XX MPI: 2003-174098/17.
DR N-PSDB; ABX89495.
XX
XX New secreted and transmembrane polypeptides (e.g. PRO241, for use in
PT pharmaceuticals, diagnostics or bioreactors, particularly for detecting
PT or treating e.g. cancers, infertility or acquired immunodeficiency
PT syndrome in mammals.
XX
XX Claim 1: Fig 32; 173pp; English.
XX
XX The invention relates to a human secreted and transmembrane polypeptide
CC (PRO) and the polynucleotide encoding it. The PRO polypeptide or
CC polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or
CC bioreactors. These are particularly useful for detecting or treating
CC cancers, inflammatory diseases, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, acquired immunodeficiency
CC syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,
CC cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are
CC also useful in biotechnological and medical research and in various
CC industrial applications. Sequences AB060230-AB060245 represent human PRO
CC polypeptides of the invention
XX
XX Sequence 431 AA;
SQ
Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,6e-173; Indels 0; Gaps 0;
Matches 431; Conservative 0; Mismatches 0;
QY 1 MFFGGSGSLTYLTIVICFLTLRLASQNCLEEDVVIDIOSLSKGRNEPVYTSQ 60
Db 1 MFFGGSGSLTYLTIVICFLTLRLASQNCLEEDVVIDIOSLSKGRNEPVYTSQ 60
QY 61 EDCINSCSTKNISGKACNLMIPTDRTKTAQPCNYLFCPNEACPLKPAKGLMSYRII 120
Db 61 EDCINSCSTKNISGKACNLMIPTDRTKTAQPCNYLFCPNEACPLKPAKGLMSYRII 120
QY 121 TDFPSTLRLPSEQLPQEDSLHGFQSOAVTPLAHHHTYSKPTDISMDTSLQKRGSSD 180
Db 121 TDFPSTLRLPSEQLPQEDSLHGFQSOAVTPLAHHHTYSKPTDISMDTSLQKRGSSD 180
QY 181 HLEKLFKMDASQQLAAVEKKGSSQSSDOEIHLLPENVSALPATVAVASPTTTA 240
Db 181 HLEKLFKMDASQQLAAVEKKGSSQSSDOEIHLLPENVSALPATVAVASPTTTA 240
QY 241 TPKPATLPTNASVTPSGTSQPLATAPVTTVTSQPTTLISTVFTRAAATLQAMAT 300
Db 241 TPKPATLPTNASVTPSGTSQPLATAPVTTVTSQPTTLISTVFTRAAATLQAMAT 300
QY 301 AVLTTFQAPDTSGKSLFTIPFEISNLNTNGVNPFPALSMNSVESTNMTASWEGR 360
Db 301 AVLTTFQAPDTSGKSLFTIPFEISNLNTNGVNPFPALSMNSVESTNMTASWEGR 360
QY 361 EASPGSSSQSVENQYGLPFEKMLIGSLFGVLFLVGLVGLIGRIILBSRLARKKYSRL 420
Db 361 EASPGSSSQSVENQYGLPFEKMLIGSLFGVLFLVGLVGLIGRIILBSRLARKKYSRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

RESULT 14
ABU72590
ID ABU72590 standard; protein; 431 AA.
XX
XX AC ABU72590;
XX
XX DT 17-JUN-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO361.
XX
XX Human; secreted and transmembrane protein; cytostatic; anti-HIV,
KW vitucide; hepatocytic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening.
XX
XX OS Homo sapiens.
XX
XX PN US2003003531-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 19-NOV-2001; 2001US-00989734.
XX
XX PR 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 05-NOV-1997; 97WO-0062006P.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PR 20-MAR-1998; 98US-0078910P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 28-MAY-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088025P.
XX PR 04-JUN-1998; 98US-0088026P.
XX PR 04-JUN-1998; 98US-0088028P.
XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.
XX PR 04-JUN-1998; 98US-0088326P.
XX PR 05-JUN-1998; 98US-0088167P.
XX PR 05-JUN-1998; 98US-0088202P.
XX PR 05-JUN-1998; 98US-0088212P.
XX PR 05-JUN-1998; 98US-0088217P.
XX PR 09-JUN-1998; 98US-0088655P.
XX PR 10-JUN-1998; 98US-0088734P.
XX PR 10-JUN-1998; 98US-0088738P.
XX PR 10-JUN-1998; 98US-0088742P.
XX PR 10-JUN-1998; 98US-0088810P.
XX PR 10-JUN-1998; 98US-0088824P.
XX PR 10-JUN-1998; 98US-0088826P.
XX PR 11-JUN-1998; 98US-0088858P.
XX PR 11-JUN-1998; 98US-0088861P.
XX PR 11-JUN-1998; 98US-0088876P.
XX PR 12-JUN-1998; 98US-0089105P.
XX PR 16-JUN-1998; 98US-0089440P.
XX PR 16-JUN-1998; 98US-0089512P.
XX PR 16-JUN-1998; 98US-0089514P.
XX PR 17-JUN-1998; 98US-0089532P.
XX PR 17-JUN-1998; 98US-0089538P.
XX PR 17-JUN-1998; 98US-0089598P.
XX PR 17-JUN-1998; 98US-0089599P.
XX PR 17-JUN-1998; 98US-0089600P.
XX PR 17-JUN-1998; 98US-0089633P.

PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017806.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,
PI Ferrara N, Fong S, Gerber H, Gerltsen ME, Goddard A, Godowski PJ,
PI Grijalvaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Peoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WJ,
PI Zhang Z;
XX
XX WPI; 2003-352829/33.
DR N-PSDB; ACN64519.
XX
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
XX
XX Claim 12; Fig 328; 663bp; English.
XX
XX
XX The invention describes a new isolated nucleic acid molecule comprising
XX the full length coding sequence of the DNA deposited with the American
XX Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
XX 209439, 201335, etc.) or a sequence with at least 80% identity to a DNA
XX encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
XX useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
XX are particularly useful for detecting or treating e.g. malignancies or
XX cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,

CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 431 AA;
Query Match 100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.6e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFPGGSLTYTVICFLTLRLASQCLKSLLEDVVIDISSLSSKIRGNRPVYSTQ 60
DB 1 MFPGGSLTYTVLVCFLTLRLASQCLKSLLEDVVIDISSLSSKIRGNRPVYSTQ 60
QY 61 EDCINSCSTKNISGDKACNIMIPDTRKTAQPNCYLFCFENBEACPLKPAKGLMSYRII 120
DB 61 EDCINSCSTKNISGDKACNIMIPDTRKTAQPNCYLFCFENBEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTNNLPSQELPQEDSLHGFQSOAVTPLAHHTDYKPTDISWRDTLSQKFGSSD 180
DB 121 TDFPSLTNNLPSQELPQEDSLHGFQSOAVTPLAHHTDYKPTDISWRDTLSQKFGSSD 180
QY 181 HLEKLFKMDKSAQOLAYKKGHSQSSQSSDOEIAHLIPNVSAALPTVAVASHTTSA 240
DB 181 HLEKLFKMDKSAQOLAYKKGHSQSSQSSDOEIAHLIPNVSAALPTVAVASHTTSA 240
QY 241 TPKPATLLPTNASVTPSGTSPOLATTAPPYTVTVSQPPTLISVFTRAATLQAMATT 300
DB 241 TPKPATLLPTNASVTPSGTSPOLATTAPPYTVTVSQPPTLISVFTRAATLQAMATT 300
QY 301 AVLTTFQAPLPDSKGSLETTIPFTEISNLTNTGVNVPALSMNSVSSSTMNKTASWEGR 360
DB 301 AVLTTFQAPLPDSKGSLETTIPFTEISNLTNTGVNVPALSMNSVSSSTMNKTASWEGR 360
QY 361 EASPGSSQSSVPENQVGLPPEKMLIGSLFLGVFLVIGLVGLGRILSESLLRRRYSRL 420
DB 361 EASPGSSQSSVPENQVGLPPEKMLIGSLFLGVFLVIGLVGLGRILSESLLRRRYSRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431
RESULTE 15
ABU64930
ID ABU64930 standard; protein; 431 AA.
XX
XX AC ABU64930;
XX
XX DT 15-MAY-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO361.
XX
XX KW Human; PRO; secreted protein; transmembrane protein;
XX Corneille de Lange syndrome; gene therapy; immune disorder;
XX inflammatory disease; organ failure; atherosclerosis; cardiac injury;
XX infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
XX diabetic complication.
OS Homo sapiens.
XX
XX PN US2002173463-A1.
XX
XX PD 21-NOV-2002.
XX
XX PF 31-AUG-2001; 2001US-00944944.

XX 03-DEC-1997; 97US-0067411P.
 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 16-DEC-1997; 97US-0069696P.
 PR 16-DEC-1997; 97US-0069702P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 17-DEC-1997; 97US-0069873P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 05-JAN-1998; 98US-0070440P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-0112966P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 28-JUL-1999; 99US-0146222P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Baker KP, Boetstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
 PI Hillan KJ, Kijavyn IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 XX WPI: 2003-311003/30.
 DR N-PSDB; ABX96832.
 PT
 PT New transmembrane polypeptides and polynucleotides useful for chromosome
 PT identification, tissue typing, gene therapy, in chromosome and gene
 PT mapping, or as molecular weight markers.
 XX
 PS Claim 12; Fig 32; 172pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted/
 CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
 CC polypeptides and their encoding polynucleotides are disclosed. Also
 CC included are a vector comprising the PRO nucleic acid, a host cell
 CC comprising the vector, a process for producing a PRO polypeptide (by
 CC culturing the host cell under conditions for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
 CC isolated polypeptide having at least 80% amino acid sequence identity to
 CC the PRO polypeptides, a chimeric molecule comprising PRO fused to a
 CC heterologous amino acid sequence and an antibody which specifically binds
 CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
 CC in chromosome and gene mapping, in generating sense and antisense RNA or
 CC DNA, in generating transgenic or knock-out animals which can be used in
 CC the development and screening of therapeutically useful reagents, and in
 CC gene therapy. The polypeptides may be used as molecular weight markers
 CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
 CC acids may also be used for chromosome identification, and tissue typing.
 CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
 CC syndrome. Other PRO proteins are variously implicated in immune
 CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
 CC injury, infertility, birth defects, premature aging, cardiac injury.

CC AIDS, cancer and diabetic complications. The present sequence represents
 CC a PRO protein
 XX
 SQ Sequence 431 AA;
 Query Match 100.0%; Score 2211; DB 6; Length 431;
 Best Local Similarity 100.0%; Pred. No. 3.6e-173;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFPGEGSLTYTVVICFLTRLASQNCLEKSLIEDVVIDIQSSLSKGRNGNEPVYTQ 60
 DB 1 MFPGEGSLTYTVVICFLTRLASQNCLEKSLIEDVVIDIQSSLSKGRNGNEPVYTQ 60
 QY 61 EDCINSCSTKNISGDKACNMIFDTRKTAQPCNYLFCFNEEACPLKPAKGLMSYRII 120
 DB 61 EDCINSCSTKNISGDKACNMIFDTRKTAQPCNYLFCFNEEACPLKPAKGLMSYRII 120
 QY 121 TDFPSLTNLPQSELPOEDSLHGFQFQAVTPPLAHHRTDYKFPDLSWRDTLSQKFGSSD 180
 DB 121 TDFPSLTNLPQSELPOEDSLHGFQFQAVTPPLAHHRTDYKFPDLSWRDTLSQKFGSSD 180
 QY 181 HLEKLFKMDKASAOQLAYKEKGHSQSOSFSSDOETAHLLPENVSALPATVAASPHTTSA 240
 DB 181 HLEKLFKMDKASAOQLAYKEKGHSQSOSFSSDOETAHLLPENVSALPATVAASPHTTSA 240
 QY 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPYTVTSQPTTLISVFTRAATLQAMATT 300
 DB 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPYTVTSQPTTLISVFTRAATLQAMATT 300
 QY 301 AVLTTTPAAPTDSKGSLETFTEISNLTMTGNYNPTALSMGVESSTYNNKTAASWGR 360
 DB 301 AVLTTTPAAPTDSKGSLETFTEISNLTMTGNYNPTALSMGVESSTYNNKTAASWGR 360
 QY 361 EASPGSSQGSVPENQYGLPEKMLLIGSLFGVLFVIGLVLAGRIISESLRRKRSRL 420
 DB 361 EASPGSSQGSVPENQYGLPEKMLLIGSLFGVLFVIGLVLAGRIISESLRRKRSRL 420
 QY 421 DYLINGIYVDI 431
 DB 421 DYLINGIYVDI 431

Search completed: April 28, 2004, 12:57:51
 Job time : 63 secs

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OM protein - protein search, using sw model

Run on: April 28, 2004, 12:56:43 ; Search time 23 Seconds

(without alignments)
967.426 Million cell updates/sec

Title: US-10-677-471-83

Perfect score: 2211

Sequence: 1 MFPGGSGSLTYLVIIICFLT.....LRRKRYSLDYINGIYVDI 431

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	431	4	US-09-866-028-83
2	183	8.3	266	4	US-09-489-847-332
3	145.5	6.6	629	4	US-09-241-581B-6
4	145.5	6.6	629	4	US-08-265-428-6
5	145.5	6.6	629	5	PCT-US95-07721-6
6	129	5.8	175	3	US-08-700-651-12
7	129	5.8	175	3	US-08-928-361B-17
8	129	5.8	175	3	US-09-588-995A-11
9	128	5.8	249	3	US-08-700-651-15
10	128	5.8	249	3	US-08-928-361B-20
11	128	5.8	249	4	US-09-588-995A-20
12	127.5	5.7	1601	4	US-09-345-473B-40
13	127	5.7	288	4	US-09-216-393B-341
14	127	5.7	288	4	US-09-216-393B-344
15	127	5.7	357	1	US-08-078-683A-8
16	127	5.7	357	4	US-08-471-970A-8
17	126.5	5.7	1837	3	US-08-928-361B-5
18	126.5	5.7	1837	4	US-09-556-706B-2
19	126	5.7	878	4	US-09-588-995A-5
20	125.5	5.7	1721	3	US-08-700-651-5
21	125.5	5.7	1721	3	US-08-928-361B-6
22	125.5	5.7	1721	4	US-09-588-995A-6
23	125	5.7	2137	4	US-09-134-001C-4463
24	124.5	5.6	451	1	PCT-US95-09941-2
25	124.5	5.6	451	5	PCT-US95-09941-2
26	123.5	5.6	806	1	US-08-270-076A-11
27	123	5.6	150	3	US-08-928-361B-18

28	123	5.6	150	4	US-09-588-995A-18	Sequence 18, Appl
29	123	5.6	216	3	US-08-928-361B-27	Sequence 27, Appl
30	123	5.6	334	4	US-09-197-970B-7	Sequence 7, Appl
31	121.5	5.5	216	3	US-08-928-361B-8	Sequence 8, Appl
32	121.5	5.5	216	4	US-09-588-995A-8	Sequence 4, Appl
33	121	5.5	750	4	US-09-165-239A-4	Sequence 4, Appl
34	120.5	5.5	162	3	US-08-700-651-13	Sequence 13, Appl
35	119	5.4	138	3	US-08-700-651-10	Sequence 10, Appl
36	119	5.4	138	3	US-08-928-361B-15	Sequence 15, Appl
37	119	5.4	138	4	US-09-588-995A-15	Sequence 15, Appl
38	119	5.4	401	6	5252556-1	Patent No. 5252556
39	119	5.4	786	3	US-09-103-429A-3	Sequence 3, Appl
40	119	5.4	805	3	US-09-103-429A-4	Sequence 3, Appl
41	118.5	5.4	521	1	US-08-276-213-3	Sequence 9, Appl
42	118	5.3	789	4	US-08-971-188-9	Sequence 22, Appl
43	118	5.3	789	4	US-09-374-454-22	Sequence 22, Appl
44	118	5.3	907	3	US-08-783-774-2	Sequence 1, Appl
45	118	5.3	907	4	US-09-328-599A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-866-028-83

; Sequence 83, Application US/09866028

; Patent No. 6642360

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Baton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gueney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/866, 028

; CURRENT FILING DATE: 2001-05-25

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 83

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-09-866-028-83

Query Match 100.0%; Score 2211; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-202;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPGGSGSLTYLVIIICFLTSLASONCKLSLDDVVDIOSLSKIRGNEPYTSTQ 60
DB 1 MFPGGSGSLTYLVIIICFLTSLASONCKLSLDDVVDIOSLSKIRGNEPYTSTQ 60
QY 61 EDCINSCCSTKNISGDKACNLMIPTRTKTAROPNCYLFECPEBEACPLKPAKGLMSYRII 120
DB 61 EDCINSCCSTKNISGDKACNLMIPTRTKTAROPNCYLFECPEBEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRNLPSQELPQEDSLIHGQPSQAVTPPLAHHHTDYSKPTDI SWRDTLSQKFGSSD 180
DB 121 TDFPSLTRNLPSQELPQEDSLIHGQPSQAVTPPLAHHHTDYSKPTDI SWRDTLSQKFGSSD 180

QY 181 HLEKLFKNDDEASAOQLAYKEKHSQSSQPSDQETIAHLIPENVASLPATVAVASPHTTSA 240
Db 181 HLEKLFKNDDEASAOQLAYKEKHSQSSQPSDQETIAHLIPENVASLPATVAVASPHTTSA 240
QY 241 TPKPATLLPTNASVPSGTSQPOLATTPPVTVTSQPTTLISTVFPRAATLQAMATT 300
Db 241 TPKPATLLPTNASVPSGTSQPOLATTPPVTVTSQPTTLISTVFPRAATLQAMATT 300
QY 301 AVLTTFQAPDTSKGSLETPTEISNLTNTGNYNPALSMNSVESSTMNKTASWEGR 360
Db 301 AVLTTFQAPDTSKGSLETPTEISNLTNTGNYNPALSMNSVESSTMNKTASWEGR 360
QY 361 EASPSSSSGSVENQYGLPEFKWLLIGSLFGVLFLVGLGRILSESLRRKRSRL 420
Db 361 EASPSSSSGSVENQYGLPEFKWLLIGSLFGVLFLVGLGRILSESLRRKRSRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

RESULT 2

US-09-489-847-332
; Sequence 332; Application US/09489847

; Patent No. 6476195

; GENERAL INFORMATION:

; APPLICANT: Rosen et al

; TITLE OF INVENTION: 98 Human Secreted Proteins

; FILE REFERENCE: P2031P1

; CURRENT APPLICATION NUMBER: US/09/489, 847

; EARLIER FILING DATE: 2000-01-24

; EARLIER APPLICATION NUMBER: PCT/US99/17130

; EARLIER FILING DATE: 1999-07-29

; EARLIER APPLICATION NUMBER: 60/094,657

; EARLIER FILING DATE: 1998-07-30

; EARLIER APPLICATION NUMBER: 60/095,486

; EARLIER FILING DATE: 1998-08-05

; EARLIER APPLICATION NUMBER: 60/096,319

; EARLIER FILING DATE: 1998-08-12

; EARLIER APPLICATION NUMBER: 60/095,454

; EARLIER FILING DATE: 1998-08-06

; EARLIER APPLICATION NUMBER: 60/095,455

; EARLIER FILING DATE: 1998-08-06

; NUMBER OF SEQ ID NOS: 376

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 332

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (97)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (174)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (199)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (195)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (206)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; US-09-489-847-332

Query Match 8.3%; Score 183; DB 4; Length 266
Best Local Similarity 27.2%; Pred. No. 3.8e-09;

Matches 80; Conservative 42; Mismatches 116; Indels 56; Gaps 13;
QY 158 TDYSPKTDISWRDLTQKFGSSDHLKLFKNDDEASAOQLAYKEKHSQSSQPSDQETIAH 217
Db 5 TEDSRDTVSESPATSG---GAADGVTSIAPFAVASSTTAA-----SITTAASMTVA 54
QY 218 LLPENVASLPATVAVASPHT-----TSATPPATL-LPTNASV-----TPS--GTSQPOLA 265
Db 55 SAP--TTAASSTTVASIAPTTASMTAASSTPMTLALPAPSTYGTGRPSSTATGHPSL 113
QY 266 TPAPVTVTSQPTTLISTVFPRAATLQAMATTAVLTTFQA--PTDSKGSLETPTE 324
Db 114 TALAQPKSSALPRTATLATTATRA---QTVAITANTSSPMSTRPSSKMPSTTASP 169
QY 325 ISNLTNTGNYNPAL--LSMSNVESSTMNKTASWEGREASPGSSQSGSVENQYGLPF 381
Db 170 VPPMX-----PQAGPISQSVDPQVAVTT-----XKSTXPSNTTXPL 209
QY 382 -----EKLWLLIGSLFGVLFLVGLGRILSESLRRKRSRLDYLINGIYVD 430
Db 210 TQAVVDKTLVLVLLGVTLFTVLVLPALQAYESYKKKDYTOVDYLINGMYAD 263

RESULT 3

US-09-241-581B-6
; Sequence 6, Application US/09241581B

; Patent No. 6350859

; GENERAL INFORMATION:

; APPLICANT: Massachusetts Institute of Technology

; TITLE OF INVENTION: Class BI and CI Scavenger Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patricia L. Pabst

; STREET: 2800 One Atlantic Center

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/241,581B

; FILING DATE: 02-Feb-1999

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patricia L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: M16620

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794

; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 629 amino acids

; TYPE: amino acid

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal

; FEATURE:

; NAME/KEY: misc. feature

; LOCATION: 1..629

; OTHER INFORMATION: /Function = "Amino acid sequence for the

; Drosophila Melanogaster Scavenger Receptor

; Class CI."

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 30..353

; OTHER INFORMATION: /note= "Positions 30-32, 90-92,

```

Query March          6.6%; Score 145.5; DB 4; Length 629;
Best Local Similarity 22.9%; Pred. No. 5.7e-05;
Matches 48; Conservative 30; Mismatches 79; Indels 53; Gaps 5;

QY      213 QEIAHLPEVNSALPATVAASPH-----TSATPKPAILLPITNASVTSGTSG 261
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      383 KEILTTTEDDISSLPTIVSTSTSRKSTTTTTTSTSTSTTKRPTTTTTTKATTY 442
QY      262 PQIATTAPPVTVTSQPPTLLISTVFRAAIIQAMATTAVLTTRQAPIDSKSLETIP 321
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      443 KRITTTKKPPTTSTTPKPPTTSTTPKSTSTSTSTSTPTTTTINVFYTK----- 495
QY      322 FTEISNLTLTNGVYNFTALSMNSVSSSTMNKTAWS-----EGREASPSSSQGSVE 374
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      496 ----TTMTTTSSEKTGTG----ITTMKRKAITMNVDPDIEGHMDTGSTPNPALV- 546
QY      375 NQYGLPPEKWLIGSLDFVLPLVIGLVLL 404
       ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      547 -----VLVIILLGIIVL 557

RESULT 4
US-08-265-428--6
Sequence 6, Application US/08265428
Patent No. 6429289
GENERAL INFORMATION:
APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Scavenger Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,428
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..629
OTHER INFORMATION: /Function = "amino acid sequence for the Drosophila Melanogaster"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30..353
OTHER INFORMATION: /note= "positions 30-32, 90-92,
OTHER INFORMATION: 129-131, 180-182, 253-255 and 351-353 represent
OTHER INFORMATION: potential N-glycosylation sites."
FEATURE:
NAME/KEY: Modified-site

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LOCATION: 1..20 /note= "Amino acids 1-20 represent
OTHER INFORMATION: a putative signal sequence."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..74 /note= "Amino acids 21-74 represent
OTHER INFORMATION: complement control protein domain number 1."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 75..127 /note= "Amino acids 75-127
OTHER INFORMATION: represent complement control protein domain number
OTHER INFORMATION: 2."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 128..312 /note= "Amino acids 128-312
OTHER INFORMATION: represent an MAM domain."
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 22..381 /note= "The cysteines at positions
OTHER INFORMATION: 22, 45, 59, 72, 77, 99, 113, 123, 136, 144, 216,
OTHER INFORMATION: 217, 254, 310, 339, 343, 361, 367, 373, 374 and 381
OTHER INFORMATION: represent potential disulfide linkages."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 338..381 /note= "Amino acids 338-381
OTHER INFORMATION: represent a somatomedin B domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 387..514 /note= "Amino acids 387-514
OTHER INFORMATION: represent a mucin-like potential O-linked
OTHER INFORMATION: glycosylation region."
FEATURE:
NAME/KEY: Domain
LOCATION: 544..564 /note= "Amino acids 544-565
OTHER INFORMATION: represent a putative TM domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 565..629 /note= "Amino acids 565-629
OTHER INFORMATION: represent a putative cytoplasmic domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 576..602 /note= "Amino acids 576-579 and
OTHER INFORMATION: 599-602 represent casein kinase II sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 578..592 /note= "Amino acids 578-580 and
OTHER INFORMATION: 590-592 represent protein kinase C sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 596..599 /note= "Amino acids 596-599
OTHER INFORMATION: represent a CAMP protein kinase site."
US-08-265-428-6
Query Match 6.6%; Score 145.5; DB 4; Length 629;
Best Local Similarity 22.9%; Pred. No. 5.7e-05;
Matches 48; Conservative 30; Mismatches 79; Indels 53; Gaps 5;
Qy 213 OEIAHLLENVSALEPATVAVASPHT-----TSATPKPALLLPTNMSVTPSGNSQ 261
Db 383 KEULTTEDDISLSPVTVSTSTTRKSTTTTSTTTSTTTTKRPPTTTTKATTT 442
Qy 262 POLATAPPVTTVTQPTTLTSTVETRAAATLQAMATTAVLTTFQAPTDSKSLETIP 321

Db 443 KRITTKKPTTSTTPKPTTSTTPKSTSTSTSTSTPTTTTINVFTTK----- 495
Qy 322 FTEISNLTNTNGVYNNPALSMSNVESITNKTASW-----GGRASPGSSGGSVPE 374
Db 496 ---TTIWTPTSSTEKTTGI---ITTWKTKRKRTTMVNDPODIGHMDTSGSTPNPALV- 546
Qy 375 NQYGLPEFKWLLIGSLFGLVFLVIGLVLL 404
Db 547 -----VLYLLGIVLV 557
RESULT 5
PCT-US95-07721-6
Sequence 6, Application PC/TUS9507721
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07721
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..629 /function = "Amino acid sequence for the
OTHER INFORMATION: Drosophila Melanogaster Scavenger Receptor
OTHER INFORMATION: Class CI."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30..353 /note= "Positions 30-32, 90-92,
OTHER INFORMATION: 129-131, 180-182, 253-255 and 351-353
OTHER INFORMATION: represent potential N-glycosylation
OTHER INFORMATION: sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..20 /note= "Amino acids 1-20 represent
OTHER INFORMATION: a putative signal sequence."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..74 /note= "Amino acids 21-74 represent

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OTHER INFORMATION: complement control protein domain
FEATURE: number 1."
NAME/KEY: Modified-site
LOCATION: 75..127 /note="Amino acids 75-127
OTHER INFORMATION: represent complement control protein
OTHER INFORMATION: domain number 2."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 128..312 /note="Amino acids 128-312
OTHER INFORMATION: represent an MAM domain."
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 22..381
OTHER INFORMATION: /note="The cysteines at positions
OTHER INFORMATION: 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216,
OTHER INFORMATION: 217, 254, 310, 339, 343, 361, 363, 367, 373, 374
OTHER INFORMATION: and 381 represent potential disulfide linkages."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 338..381 /note="Amino acids 338-381
OTHER INFORMATION: represent a somatomedin B domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 387..514 /note="Amino acids 387-514
OTHER INFORMATION: represent a mucin-like potential
OTHER INFORMATION: O-linked glycosylation region."
FEATURE:
NAME/KEY: Domain
LOCATION: 544..564 /note="Amino acids 544-565
OTHER INFORMATION: represent a putative TM domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 565..629 /note="Amino acids 565-629
OTHER INFORMATION: represent a putative cytoplasmic
OTHER INFORMATION: domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 576..602 /note="Amino acids 576-579 and
OTHER INFORMATION: 599-602 represent casein kinase II
OTHER INFORMATION: sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 578..592 /note="Amino acids 578-580 and
OTHER INFORMATION: 590-592 represent protein kinase C
OTHER INFORMATION: sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 596..599 /note="Amino acids 596-599
OTHER INFORMATION: represent a CAMP protein kinase site."
OTHER INFORMATION:
PCT-US95-07721-6

Query Match 6.6%; Score 145.5; DB 5; Length 629;
Best Local Similarity 22.9%; Pred. No. 5.7e-05;
Matches 48; Conservative 30; Mismatches 79; Indels 53; Gaps 5;

```

```

213 OEIAHLPEVNSALPATVAVASPH-----TSATPKPATLPTNASVTPSGTSG 261
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
383 KELTTTBDISLSPPTVSTSTSRKSTTTTSTTTSTTTTTRRPTTTTTRKATTT 442
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
262 POLATTAPVTTVTSOPPTTLISIVTRRAATLQAMATTAVALTTTFOAPDTSKSLETIP 321
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
443 KRTTTTKKPTTTSTTRPKPTTTTSTTRKSTTSTSTSTSTPTTTTINVTTKK----- 495

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Qy 322 FTEISNLTNTGNVNPALMSNVESSTMNKTASW-----EGREASPGSSGGSVPE 374
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 496 ----TTIMPTSTSEKTTGI-----ITTKTRKRITWVDPQDIEGHMDTSGSTPPALV- 546
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 375 NOYGLPFEKMLIGSLFGVLPVIGVYL 404
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 547 -----VYLLGLIVLV 557
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 6

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US-08-700-651-12
; Sequence 12, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; CURRENT FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 08/415,751
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 175
; TYPE: PRF
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-12

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Query Match

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5.8%; Score 129; DB 3; Length 175;
Best Local Similarity 27.3%; Pred. No. 0.00027;
Matches 35; Conservative 15; Mismatches 74; Indels 4; Gaps 1;

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Qy 226 LPATVAVASPHTSATPKPATLPTNASVTPSGTSGPOLATTAPVTTVTSOPPTTLIST 285
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 IPYKCVGKHTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 62
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 286 VFTRRAATLQAMATTAVALTTTFOAPDTSKSLETIPFTEISNLTNTGNVNPALMSN 345
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 122
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 346 VESSTMNK 353
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 TTTTNTTK 130
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 7

```

US-08-928-361B-17
; Sequence 17, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-17

Query Match 5.8%; Score 129; DB 3; Length 175;
Best Local Similarity 27.3%; Pred. No. 0.00027;
Matches 35; Conservative 15; Mismatches 74; Indels 4; Gaps 1;
QY 226 LPATVAVASPHHTSATPKRATLLPTNASTVPSGTSQPOLATTAPVTVTSQPTTLIST 285
DB 7 IPYKCVGKHTTTTTTTTTTTTTTTTTTTTTTTT-----TTTTTTTTTTTTTTTTTTTT 62
QY 286 VETRAAATLQAMATTAVLTTFQAPTDKSGSLETIPFEISNLTLTNGVNPALSMNSN 345
DB 63 TTTTTTTTTTTTTTTTTTTTTTTTCKKPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 122
QY 346 VESSTMNK 353
DB 123 TTTTTTTK 130

RESULT 8
US-09-588-995A-17
Sequence 17, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 175
TYPE: PRT
ORGANISM: Cryptosporidium parvum
US-09-588-995A-17

Query Match 5.8%; Score 129; DB 4; Length 175;
Best Local Similarity 27.3%; Pred. No. 0.00027;
Matches 35; Conservative 15; Mismatches 74; Indels 4; Gaps 1;
QY 226 LPATVAVASPHHTSATPKRATLLPTNASTVPSGTSQPOLATTAPVTVTSQPTTLIST 285
DB 7 IPYKCVGKHTTTTTTTTTTTTTTTTTTTTTTTT-----TTTTTTTTTTTTTTTTTTTT 62
QY 286 VETRAAATLQAMATTAVLTTFQAPTDKSGSLETIPFEISNLTLTNGVNPALSMNSN 345
DB 63 TTTTTTTTTTTTTTTTTTTTTTTTCKKPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 122
QY 346 VESSTMNK 353
DB 123 TTTTTTTK 130

RESULT 9
US-08-700-651-15
Sequence 15, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEBCH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 249
TYPE: PRT
ORGANISM: Cryptosporidium parvum
FEATURE:
OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-15

Query Match 5.8%; Score 128; DB 3; Length 249;
Best Local Similarity 26.0%; Pred. No. 0.00059;
Matches 34; Conservative 15; Mismatches 82; Indels 0; Gaps 0;
QY 226 LPATVAVASPHHTSATPKRATLLPTNASTVPSGTSQPOLATTAPVTVTSQPTTLIST 285
DB 7 IPYKCVGKHTTTTTTTTTTTTTTTTTTTTTTTT-----TTTTTTTTTTTTTTTTTTTT 66
QY 286 VETRAAATLQAMATTAVLTTFQAPTDKSGSLETIPFEISNLTLTNGVNPALSMNSN 345
DB 67 TTTTTTTTTTTTTTTTTTTTTTTTCKKPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 126
QY 346 VESSTMNK 356
DB 127 TTTTTTTTTT 137

RESULT 10
US-08-928-361B-20
Sequence 20, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
 ADDRESSEE: PETERS, VERNY, JONES & BIRKA
 STREET: 385 Sherman Avenue, Suite 6
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-1840
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,361B
 FILING DATE: 12-SEP-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,062
 FILING DATE: 13-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: VERNY, Hana
 REGISTRATION NUMBER: 30,518
 REFERENCE/DOCKET NUMBER: 480.76-1(HV)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-324-1677
 TELEFAX: 650-324-1678
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 249 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-928-361B-20

Query Match 5.8%; Score 128; DB 3; Length 249;
 Best Local Similarity 26.0%; Pred. No. 0.00059;
 Matches 34; Conservative 15; Mismatches 82; Indels 0; Gaps 0;
 QY 226 LPATVAVSPHTTSATPKRATLLPTNASTPBGTSQPOLATAPVTVTSQPTTLIST 285
 DB 7 IPYKCVGKHTTT 66
 QY 286 VETRAATLQAMATTAVLTTFQAPTDKSGLETIPTEISNLTLTNGVNPALSMNSN 345
 DB 67 TT 126
 QY 346 VESSTMNKTAS 356
 DB 127 TTTTTTTTTTT 137
 RESULT 11
 US-09-588-995A-20
 Sequence 20, Application US/09588995A
 Patent No. 6514697
 GENERAL INFORMATION:
 APPLICANT: PETERSEN, CAROLYN
 APPLICANT: BARNES, DEBRA A.
 APPLICANT: NELSON, RICHARD C.
 APPLICANT: GUT, JIRI
 TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
 TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
 TITLE OF INVENTION: INFECTIONS
 FILE REFERENCE: 480.19-5
 CURRENT APPLICATION NUMBER: US/09/588,995A
 CURRENT FILING DATE: 2000-06-06
 PRIOR APPLICATION NUMBER: 08/827,171
 PRIOR FILING DATE: 1997-03-27
 PRIOR APPLICATION NUMBER: 08/928,361
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: 08/700,651
 PRIOR FILING DATE: 1996-08-14

PRIOR APPLICATION NUMBER: 08/415,751
 PRIOR FILING DATE: 1995-04-03
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 20
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Cryptosporidium parvum
 US-09-588-995A-20

Query Match 5.8%; Score 128; DB 4; Length 249;
 Best Local Similarity 26.0%; Pred. No. 0.00059;
 Matches 34; Conservative 15; Mismatches 82; Indels 0; Gaps 0;

QY 226 LPATVAVSPHTTSATPKRATLLPTNASTPBGTSQPOLATAPVTVTSQPTTLIST 285
 DB 7 IPYKCVGKHTTT 66
 QY 286 VETRAATLQAMATTAVLTTFQAPTDKSGLETIPTEISNLTLTNGVNPALSMNSN 345
 DB 67 TT 126
 QY 346 VESSTMNKTAS 356
 DB 127 TTTTTTTTTTT 137

RESULT 12
 US-09-345-473E-40
 Sequence 40, Application US/09345473E
 Patent No. 6558903
 GENERAL INFORMATION:
 APPLICANT: Hodge, Martin
 TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
 FILE REFERENCE: 35800/183781
 CURRENT APPLICATION NUMBER: US/09/345,473E
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ ID NOS: 62
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 40
 LENGTH: 1601
 TYPE: PRT
 ORGANISM: C. elegans
 US-09-345-473E-40

Query Match 5.8%; Score 127.5; DB 4; Length 1601;
 Best Local Similarity 21.6%; Pred. No. 0.013;
 Matches 83; Conservative 59; Mismatches 132; Indels 111; Gaps 20;

QY 59 TQEDCINCCSTKNISGDK-----ACNLMIFPRTKTAQPNCLFPCPNEACPLKPA 111
 DB 358 TPEDLIGIRVEIKRNDADLNDLNVIEIQMLKVEDEKRRQ---YRF-----KEN 403
 QY 112 KGL-MSYRIITDPPS--LTRNLPSQELPQEDSLHGFQCAVTPLAHHHTDYSKPTDISW 168
 DB 404 EGLQFAPIENDSPDEVQOMIEQOHIPDED-----TRITTLIKXKVDAFR----- 450
 QY 169 RDTLSQKFGSSDHLKELFKMDEASAOQLIAYEKHSGSS---QPSDQETIAHLIPENVS 224
 DB 451 RD-----RDH--RLIEIKRAKEEBERIREAEIKELRLRAAKERERLEKERLE 500
 QY 225 ALPATVAVSPHTTSATPKRAT-----LLPTNASTPBGTSQPOLATTT--- 267
 DB 501 KKAATAAANPNPPIPTPATPHSSAQOPIPPPLSTQTSAAEQQS-AQQPSVAVTMTA 559
 QY 268 -APVTVTSQPTTLISTVETRAATLQAMATTAV----- 302
 DB 560 NIPAMSPISAPQPVLPSTSAVPTTMIH-VEKPSIIPQVNAVITAPVAANNVPSPP 618
 QY 303 ---LTTTFOAPTDKSGLETIPTEISNLTLTNGVNPALSMNSVSSSTM----- 351
 DB 619 APFTEDIOTPTLQONTVPRTISTDASGLVINTPASIASPSPASADVDASTAPVTPAP 678

QY 352 NKTASMEGRASPGSSSGSVENQ 376
Db 679 TPTTTTGD-----GAAASTTTEKN 698

RESULT 13
US-09-216-393B-341
; Sequence 341, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 341
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-341

Query Match
Best Local Similarity 5.7%; Score 127; DB 4; Length 288;
Matches 44; Conservative 33; Mismatches 109; Indels 22; Gaps 3;

QY 178 SSDHLEKLFKMDAS-----AQLAYKKEGHSQSOSQSSDDEIHLPE 221
Db 79 STDALDRVSQFDLVSLDLVIREAAQKFDLGRLLTIDIASGIGEGAMALMGEEAIFIRPR 138

QY 222 NVSALPATVAVASPHTTSATPKPATLPTNASVTPSGTSQPOLATTAP-PVTVTTSOPT 280
Db 139 RSKRGKKT-----TTSSSTSTSTTTTSTTTTPTTTTPTTTTPTTTTPTTTTPT 193

QY 281 TLISVTFRAAATLQAMATTAVLTTFQAPTDKSGSLPTPTPTISNLTNTGNVNPPTA 340
Db 194 TTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPT 253

QY 341 LSMNSVESSTMNKTASMEGRASPGSS 368
Db 254 TTTTPTTTTSTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPT 281

RESULT 14
US-09-216-393B-344
; Sequence 344, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 344
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-344

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Best Local Similarity 5.7%; Score 127; DB 4; Length 288;
Matches 44; Conservative 33; Mismatches 109; Indels 22; Gaps 3;

QY 178 SSDHLEKLFKMDAS-----AQLAYKKEGHSQSOSQSSDDEIHLPE 221
Db 79 STDALDRVSQFDLVSLDLVIREAAQKFDLGRLLTIDIASGIGEGAMALMGEEAIFIRPR 138

QY 222 NVSALPATVAVASPHTTSATPKPATLPTNASVTPSGTSQPOLATTAP-PVTVTTSOPT 280
Db 139 RSKRGKKT-----TTSSSTSTSTTTTSTTTTPTTTTPTTTTPTTTTPTTTTPT 193

QY 281 TLISVTFRAAATLQAMATTAVLTTFQAPTDKSGSLPTPTPTISNLTNTGNVNPPTA 340
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QY 341 LSMNSVESSTMNKTASMEGRASPGSS 368
Db 254 TTTTPTTTTSTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPT 281

RESULT 15
US-08-078-683A-8
; Sequence 8, Application US/08078683A
; Patent No. 5486599
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-08-078-683A-8

Query Match
Best Local Similarity 5.7%; Score 127; DB 1; Length 357;
Matches 67; Conservative 25; Mismatches 109; Indels 54; Gaps 11;

QY 159 DYSKPTDISWRDLSQKFGSSDHLKLFKMDASQAQLAYKKEGHSQSOSQSSDDEIHL 218
Db 41 NYERVDLE-----GSGD--DDPGDDELDD--AYGSGSGGYEQSGLETAVSL 86

QY 219 LPENVSALPATVAV-----ASPHTSAT--PK--PATLIP----- 249
Db 87 TTDTSVPLPTVAVLPVTLVQPMATPFLPTBEDTSPQQTTSVLYIPKITEAPVIPSMT 146

QY 250 ----TNASVTPSGTSQPOLATTAPVTVTSQPTTLISTVTFRAAATLQAMATTAVLT- 304
Db 147 TTAATASDSSPTS--TTTAAATTTTTTTTISTVATSKPTTQORPLPPVTKAATTR 204

Qy 305 -TTQAPTDKSGLETPTEISNLTNTGNVNPPTALSMNSVSSIMNKTASWEGREAS 363
Db 205 ATTLETPPTS--IPETSVLTVTTSRVLVPSSTAKPRSLPKPST-SRTAPTEKSTALPSS 261
Qy 364 PGSSSGSVPENQYG 378
Db 262 PTTLPTEAPQVEPG 276

Search completed: April 28, 2004, 13:00:26
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2004, 12:57:58 ; Search time 48 Seconds
(without alignments)
2488.931 Million cell updates/sec

Title: US-10-677-471-83

Perfect score: 2211

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2211	100.0	431	US-09-866-028-83	Sequence 83, Appl
2	2211	100.0	431	US-09-989-722-515	Sequence 515, App
3	2211	100.0	431	US-09-989-723-515	Sequence 515, App
4	2211	100.0	431	US-09-989-729-515	Sequence 515, App
5	2211	100.0	431	US-09-989-727-515	Sequence 515, App
6	2211	100.0	431	US-09-944-449-83	Sequence 83, Appl
7	2211	100.0	431	US-09-989-731-515	Sequence 515, App
8	2211	100.0	431	US-09-944-457-83	Sequence 83, Appl
9	2211	100.0	431	US-09-989-732-515	Sequence 515, App
10	2211	100.0	431	US-09-991-073-515	Sequence 515, App
11	2211	100.0	431	US-09-945-587-83	Sequence 83, Appl
12	2211	100.0	431	US-09-990-442-515	Sequence 515, App
13	2211	100.0	431	US-09-991-163-515	Sequence 515, App
14	2211	100.0	431	US-09-945-015-83	Sequence 83, Appl
15	2211	100.0	431	US-09-945-015-83	Sequence 83, Appl

16	2211	100.0	431	US-09-944-386-83	Sequence 83, Appl
17	2211	100.0	431	US-09-944-097-83	Sequence 83, Appl
18	2211	100.0	431	US-09-993-604-515	Sequence 515, App
19	2211	100.0	431	US-09-990-456-515	Sequence 515, App
20	2211	100.0	431	US-09-944-432-83	Sequence 83, Appl
21	2211	100.0	431	US-09-943-762-83	Sequence 83, Appl
22	2211	100.0	431	US-09-943-654-83	Sequence 83, Appl
23	2211	100.0	431	US-09-989-721-515	Sequence 515, App
24	2211	100.0	431	US-09-943-851A-83	Sequence 83, Appl
25	2211	100.0	431	US-09-944-413-83	Sequence 83, Appl
26	2211	100.0	431	US-09-992-558-515	Sequence 515, App
27	2211	100.0	431	US-09-944-403-83	Sequence 83, Appl
28	2211	100.0	431	US-09-944-896-83	Sequence 83, Appl
29	2211	100.0	431	US-09-944-944-83	Sequence 83, Appl
30	2211	100.0	431	US-09-989-293A-515	Sequence 515, App
31	2211	100.0	431	US-09-989-735-515	Sequence 515, App
32	2211	100.0	431	US-09-990-444-515	Sequence 515, App
33	2211	100.0	431	US-09-944-929-83	Sequence 83, Appl
34	2211	100.0	431	US-09-991-181-515	Sequence 515, App
35	2211	100.0	431	US-09-989-730-515	Sequence 515, App
36	2211	100.0	431	US-09-944-907-83	Sequence 83, Appl
37	2211	100.0	431	US-09-990-436-515	Sequence 515, App
38	2211	100.0	431	US-09-993-687-515	Sequence 515, App
39	2211	100.0	431	US-09-989-734-515	Sequence 515, App
40	2211	100.0	431	US-09-997-653-515	Sequence 515, App
41	2211	100.0	431	US-09-993-667-515	Sequence 515, App
42	2211	100.0	431	US-09-997-428-515	Sequence 515, App
43	2211	100.0	431	US-09-997-666-515	Sequence 515, App
44	2211	100.0	431	US-09-990-438-515	Sequence 515, App
45	2211	100.0	431	US-09-990-562-515	Sequence 515, App

ALIGNMENTS

RESULT 1
US-09-866-028-83
; Sequence 83, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-866-028-83

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFPGSGSLTYTVLIIICELTLRLSASQNCLEKSLDEVDVIDIOSSLSKGI RGN EPTVYSTQ 60
QY 61 EDCINSCSTKNI SCDKACNMI PPTRTAROPNCYL PFCBPWEACPLKPAKGLMSYRII 120
Db 61 EDCINSCSTKNI SCDKACNMI PPTRTAROPNCYL PFCBPWEACPLKPAKGLMSYRII 120
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Db 121 TDFPSELTLNLPSEQLPQEDSLHGOFSQAVTBLAHHTDYSKPTDISMRDLSQKFGSSD 180
QY 181 HLEKLPKDEASAOULLAYEKCHSOSQSPSQDEIAHLIPENVSLPATVAASPHTTSA 240
Db 181 HLEKLPKDEASAOULLAYEKCHSOSQSPSQDEIAHLIPENVSLPATVAASPHTTSA 240
QY 241 TPKPATLPTNASVPSGSPQLATTAAPVTVTVSQPPTLISVTFRAAATLOAMATT 300
Db 241 TPKPATLPTNASVPSGSPQLATTAAPVTVTVSQPPTLISVTFRAAATLOAMATT 300
QY 301 AVLTTTFOAPTDSKSL ETI PTEISNLTANTGNVNPALSMNVESSTWTKTASWEGR 360
Db 301 AVLTTTFOAPTDSKSL ETI PTEISNLTANTGNVNPALSMNVESSTWTKTASWEGR 360
QY 361 EASPSGSSQGSVPENQYGLPFEKMLLIGSLFGVLFLVIGVLGRILSESIRRRYSRL 420
Db 361 EASPSGSSQGSVPENQYGLPFEKMLLIGSLFGVLFLVIGVLGRILSESIRRRYSRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

RESULT 2

US-09-989-722-515
; Sequence 515, Application US/09989722
; Patent No. US2002072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514

	Query Match	100.0%;	Score 2211;	DB 9;	Length 431;
	Best Local Similarity	100.0%;	Pred. No. 1,3e-179;		
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DB	61	EDCINSCCSTKXISGDKACNLMIPTRKTAQPNICYLFCPCNEACPLKRAKGLMSYRII	120		
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QY	421	DYLINGIYVDI 431			
DB	421	DYLINGIYVDI 431			
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Sequence 515, Application US/09989723					
Patent No. US20020072092A1					
GENERAL INFORMATION:					
APPLICANT: Ashkenazi, Avi J.					
APPLICANT: Baker, Kevin P.					
APPLICANT: Botstein, David					
APPLICANT: Desnoyers, Luc					
APPLICANT: Eaton, Dan L.					
APPLICANT: Ferrara, Napoleone					
APPLICANT: Fong, Sherman					
APPLICANT: Gerber, Hanspeter					
APPLICANT: Gerlitsen, Mary E.					
APPLICANT: Goddard, Audrey					
APPLICANT: Godowski, Paul J.					
APPLICANT: Grimaldi, J. Christopher					
APPLICANT: Gurney, Austin L.					
APPLICANT: Kijavina, Ivar J.					

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730pic62
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-179;

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGGEGSLTYTLVLIICFLTLRLSASONCLKSLSEVDVIDIOSLSKGRNEPVYTSQ 60
DB 1 MFFGGEGSLTYTLVLIICFLTLRLSASONCLKSLSEVDVIDIOSLSKGRNEPVYTSQ 60
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DB 61 EDCINSCSTKNISGDKACNLMIFDTRKTAROPNCYLFFCPNBEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRLPSOEKPOEDSLHGOFSOAVTPLAHHTYTSKPTDISMDTISOKFGSSD 180
DB 121 TDFPSLTRLPSOEKPOEDSLHGOFSOAVTPLAHHTYTSKPTDISMDTISOKFGSSD 180
QY 181 HLEKLFKMDKDEASAOQLLAYEKHSGSOSQPSDOEIAHLHPENVASLPATVAASPHTTSA 240
DB 181 HLEKLFKMDKDEASAOQLLAYEKHSGSOSQPSDOEIAHLHPENVASLPATVAASPHTTSA 240
QY 241 TPKPATLPLTNASVTPSGTSOPOLATTPAPVTTVTSQPTTLISVFTRAAATLQAMATT 300
DB 241 TPKPATLPLTNASVTPSGTSOPOLATTPAPVTTVTSQPTTLISVFTRAAATLQAMATT 300
QY 301 AVLTTTFOAPTDKSGSLFTIIPTEISNLTLNNGVNNPFLMSNVESSTNMKTASWEER 360
DB 301 AVLTTTFOAPTDKSGSLFTIIPTEISNLTLNNGVNNPFLMSNVESSTNMKTASWEER 360
QY 361 EASPSGSSGQSVPENQYGLPFPEKMLIGSLFGVLFLVIGLVLGRILSESILRRKRYSL 420
DB 361 EASPSGSSGQSVPENQYGLPFPEKMLIGSLFGVLFLVIGLVLGRILSESILRRKRYSL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

RESULT 4
US-09-989-279-515
; Sequence 515, Application US/09989279
; Patent No. US2002072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C56
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179; Indels 0; Gaps 0;
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Qy 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431
RESULT 5
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Sequence 515 Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/089600

PRIOR FILING DATE: December 3, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
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PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
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PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
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PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
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PRIOR FILING DATE: February 11, 2000
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PRIOR FILING DATE: March 2, 2000
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PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 26, 2001

NUMBER OF SEQ ID NOS: 120
SEQ ID NO 83
LENGTH: 431
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-449-83
Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFFGEGSLTYTLVLIICFLTRLASQNCCLKSLSDVVIDIQSLSKGIRGNEPVYSTQ 60
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DB 181 HLEKLFKMDDEASQQLLAYKEKHSQSSQSSDQEIHAHLLENVSALPATVAVASPHTTSA 240
QY 241 TPKPATLLPTNASVTPSGTSPQALTTAPPTVTTYSOPTTLISVTFPRAAATLQAMATT 300
DB 241 TPKPATLLPTNASVTPSGTSPQALTTAPPTVTTYSOPTTLISVTFPRAAATLQAMATT 300
QY 301 AVLTTTPQAPDPSKGSLETIPTEISNLTNTGNVYNPTALSMNSVESTNNKTASWEGR 360
DB 301 AVLTTTPQAPDPSKGSLETIPTEISNLTNTGNVYNPTALSMNSVESTNNKTASWEGR 360
QY 361 EASPPSSSSQSVPENQYGLPEKXWLLIGSLFGVLFVIGVLGRILISESLRRRYRRL 420
DB 361 EASPPSSSSQSVPENQYGLPEKXWLLIGSLFGVLFVIGVLGRILISESLRRRYRRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431
RESULT 7
US-09-989-731-515
Sequence 515, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, Nicholas F.
APPLICANT: Paoni, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Timothy A.
APPLICANT: Stewart, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/090694

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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 EDCINSCCKTNISGDKACNLMI FDRKKTARQPCNYLFCPCNEACPLKPAKGLMSYRII 120
QY 121 TDFPSLTRNLPSQELFOEDSLHGFQSAVTPPLAHHTDYSKPTDISQKFGSSD 180
DB 121 TDFPSLTRNLPSQELFOEDSLHGFQSAVTPPLAHHTDYSKPTDISQKFGSSD 180
QY 181 HLEKFLKMDKDEASAOQLAYKEKHSOSSOPSSDOELAHLLPENVSALPATVAASPTTSA 240
DB 181 HLEKFLKMDKDEASAOQLAYKEKHSOSSOPSSDOELAHLLPENVSALPATVAASPTTSA 240
QY 241 TPKPATLLPTNASVTPSGTSQPOLATTAPVTVTSQPPPTLISVFTFRAATLQAMATT 300
DB 241 TPKPATLLPTNASVTPSGTSQPOLATTAPVTVTSQPPPTLISVFTFRAATLQAMATT 300
QY 301 AVLTTTFOAPDTSKGSLETFIPTEISNLTNTGNVYNPTALSMNVESSTMNKKTASWEGR 360
DB 301 AVLTTTFOAPDTSKGSLETFIPTEISNLTNTGNVYNPTALSMNVESSTMNKKTASWEGR 360
QY 361 EASPSSSSGSVPENOYGLPFERKMLLIGSLRGVLFVLGVILGRILSESIRRRKYSRL 420
DB 361 EASPSSSSGSVPENOYGLPFERKMLLIGSLRGVLFVLGVILGRILSESIRRRKYSRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

RESULT 8
US-09-944-457-83
; Sequence 83, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan

;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gieritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kjaevlin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/944,457
;; PRIOR FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
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;; PRIOR FILING DATE: December 16, 1997
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;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020110859A1eember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313

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; PRIOR FILING DATE: No. US200201108591member 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-83

Query Match      100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      421 DYLINGIYVDI 431
DB      421 DYLINGIYVDI 431
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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerttisen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/944,862
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
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;; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
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;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 83
;; LENGTH: 431
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-862-83

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 EDCINSCGSKNIGSGKACNLMIPDTRKTARQPCYLFCEPNEBACPLKPAKGLMSYRII 120
QY 121 TFFPSTLRLPSQELPQEDSLHGFQSOAVTPLAHHHTYSKPTDISMDTISQKFGSSD 180
DB 121 TFFPSTLRLPSQELPQEDSLHGFQSOAVTPLAHHHTYSKPTDISMDTISQKFGSSD 180
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QY 241 TKPAPATLPTNASTVPSGTSQPLATTAPPVTTVTSQPTTLISTVFTRAAATLQAMATT 300
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DB 301 AVLTTTFOAPTSGSKSLFTTPTTEISNLTNTGNVYNPPLASMSNVESSTNKTASWEGR 360
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DB 361 EASPSGSSGSGVPENOYGLPFEKMLIGSLFGLVFLVIGLVLGRILSESJRRKXYSRL 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

RESULT 10
US-09-989-732-515

;; Sequence 515, Application US/09989732
;; Patent No. US20020123463A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
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;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PLC57
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TDFPSLTNNLPQSOBLPOEDSLHGFQSAVTPPLAHHTDYAKPTDISWRDTLSQKFGSSD 180
DB 121 TDFPSLTNNLPQSOBLPOEDSLHGFQSAVTPPLAHHTDYAKPTDISWRDTLSQKFGSSD 180
QY 181 HIEKLFKNDEASQOLAYKEKGHSQSSQFSSDOEIAHLHPENVSLPPTVAVASHTTSA 240
DB 181 HIEKLFKNDEASQOLAYKEKGHSQSSQFSSDOEIAHLHPENVSLPPTVAVASHTTSA 240
QY 241 TPKPATLPTNASVPSGTSOPOLATTAPPTVTYSOPPTLLISTVFTRAAATLOAMATT 300
DB 241 TPKPATLPTNASVPSGTSOPOLATTAPPTVTYSOPPTLLISTVFTRAAATLOAMATT 300

Qy 301 AVLTTFQAPTDSKSGLETFIPTEISNLTNTGNVNPALSMNSNVSSTNNKXASWEGR 360
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Db 361 EASPSGSGSVPENYGGPPEKWLIGSLFGVLPVILGRIISESLRRKXSYSL 420
Qy 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431
RESULT 11
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Sequence 515, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirey, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;;
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Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
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; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Borstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
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; APPLICANT: Godowski, Paul
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; APPLICANT: Napier, Mary
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; APPLICANT: Tunas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
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;; PRIOR FILING DATE: February 9, 1998
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;; PRIOR FILING DATE: July 28, 1999
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;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
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;; PRIOR FILING DATE: December 16, 1998
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;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
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;; PRIOR APPLICATION NUMBER: PCT/US99/28301
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;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
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;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 83
;; LENGTH: 431
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-945-587-83

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 HHEKLFKXDEASAOILAYEKSHSOSOPSSQOEIAHLIPEVNSALPATVAASHTTSA 240
QY 241 TPKPATLLPTNASVTPSGTSPQALATTAAPVTVTSOPEPTLLISTVFTRAATLQAMATT 300
Db 241 TPKPATLLPTNASVTPSGTSPQALATTAAPVTVTSOPEPTLLISTVFTRAATLQAMATT 300
QY 301 AVLTTFQAPDPSKGSLETPTEISNLTNTGNVYNPTALSMNVESSTNKTASWEGR 360
Db 301 AVLTTFQAPDPSKGSLETPTEISNLTNTGNVYNPTALSMNVESSTNKTASWEGR 360
QY 361 EASPSSSGSGSVPENQYGLPEFKMLIGSLFGVLFLVYIGVLGRILISESLRRKYSRL 420
Db 361 EASPSSSGSGSVPENQYGLPEFKMLIGSLFGVLFLVYIGVLGRILISESLRRKYSRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

RESULT 13
US-09-990-442-515
; Sequence 515, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlesen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, V. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186


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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2211; DB 9; length 431;
Best Local Similarity 100.0%; Pred.No.1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFFGGGSLTYLVIIICFTLRISASQNLKSLSDVVIDIQSSLSKGRNEPVYTSIQ 60
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        1 MFFGGGSLTYLVIIICFTLRISASQNLKSLSDVVIDIQSSLSKGRNEPVYTSIQ 60
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        |||
        61 EDCINSCSTKNISGDKACNLMI FDRKTKARQNCVLFPCPMEACPLPAKGLMSYRII 120
QY      121 TDFPSLTRNLPSQELPQEDSLHGGQSAVTPLAHHHTYSKPTDISWBDTLSQKFGSSD 180
        |||
        121 TDFPSLTRNLPSQELPQEDSLHGGQSAVTPLAHHHTYSKPTDISWBDTLSQKFGSSD 180
DB      121 TDFPSLTRNLPSQELPQEDSLHGGQSAVTPLAHHHTYSKPTDISWBDTLSQKFGSSD 180
        |||
        121 TDFPSLTRNLPSQELPQEDSLHGGQSAVTPLAHHHTYSKPTDISWBDTLSQKFGSSD 180
QY      181 HLEKXFKMDEASAOILAYEKEGHSQSSQPSDOEIAHLIPENVSAIPATVAASPTTISA 240
        |||
        181 HLEKXFKMDEASAOILAYEKEGHSQSSQPSDOEIAHLIPENVSAIPATVAASPTTISA 240
DB      181 HLEKXFKMDEASAOILAYEKEGHSQSSQPSDOEIAHLIPENVSAIPATVAASPTTISA 240
        |||
        181 HLEKXFKMDEASAOILAYEKEGHSQSSQPSDOEIAHLIPENVSAIPATVAASPTTISA 240
QY      241 TPKPATLPTNASVTPSGTSOPOLATTA PVTVTYSQPTTISTVFTFAAATLQAMATT 300
        |||
        241 TPKPATLPTNASVTPSGTSOPOLATTA PVTVTYSQPTTISTVFTFAAATLQAMATT 300
DB      241 TPKPATLPTNASVTPSGTSOPOLATTA PVTVTYSQPTTISTVFTFAAATLQAMATT 300
        |||
        241 TPKPATLPTNASVTPSGTSOPOLATTA PVTVTYSQPTTISTVFTFAAATLQAMATT 300
QY      301 AVLTTTFOAPDTSKGSLETPTEISNLTANTGVNVPALSMSNVESSTNKKTSAMEGR 360
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        301 AVLTTTFOAPDTSKGSLETPTEISNLTANTGVNVPALSMSNVESSTNKKTSAMEGR 360
DB      301 AVLTTTFOAPDTSKGSLETPTEISNLTANTGVNVPALSMSNVESSTNKKTSAMEGR 360
        |||
        301 AVLTTTFOAPDTSKGSLETPTEISNLTANTGVNVPALSMSNVESSTNKKTSAMEGR 360
QY      361 EASPGSSSGSVPENQYGLPFPEKMLIGSLFGVLFGVLGRII SESSLRKRYSRLL 420
        |||
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DB      361 EASPGSSSGSVPENQYGLPFPEKMLIGSLFGVLFGVLGRII SESSLRKRYSRLL 420
        |||
        361 EASPGSSSGSVPENQYGLPFPEKMLIGSLFGVLFGVLGRII SESSLRKRYSRLL 420
QY      421 DYLINGIYVDI 431
        |||
        421 DYLINGIYVDI 431
DB      421 DYLINGIYVDI 431
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RESULT 14
US-09-991-163-515
; Sequence 515, Application US/09991163
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeier
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
```

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; APPLICANT: Klavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPGEGSLTYTVIYICFLTRLSASQNCLEKSLIEDVVIDIQSSLKSGIKRNEPVYTSTQ 60
DB 1 MFPGEGSLTYTVIYICFLTRLSASQNCLEKSLIEDVVIDIQSSLKSGIKRNEPVYTSTQ 60
QY 61 EDCINSCSTYKISGDACNMIFDTRKTARQPCVLPFCBNEBACPLKPAKGLMSYRII 120
DB 61 EDCINSCSTYKISGDACNMIFDTRKTARQPCVLPFCBNEBACPLKPAKGLMSYRII 120
QY 121 TDFPSLTFNLPQOELPOEDSLHGOFSQAVTPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
DB 121 TDFPSLTFNLPQOELPOEDSLHGOFSQAVTPLAHHHTDYSKPTDISMRDTLSQKFGSSD 180
QY 181 HLEKLPKMDASAOULLAYKEKGHSQSSQFSSDOEIAHLLEPNVAGALPATVAVASPHTTSA 240
DB 181 HLEKLPKMDASAOULLAYKEKGHSQSSQFSSDOEIAHLLEPNVAGALPATVAVASPHTTSA 240
QY 241 TPXPATLLPTNASVTPSGTSPOLATTAPPTVTSQPTTLISTVFRAAATTQANATT 300
DB 241 TPXPATLLPTNASVTPSGTSPOLATTAPPTVTSQPTTLISTVFRAAATTQANATT 300
QY 301 AVLTTFQAPYDSGSLFTTIFTEISNLTNTGNVNPALSMNSVSSSTNKTASWEGR 360
DB 301 AVLTTFQAPYDSGSLFTTIFTEISNLTNTGNVNPALSMNSVSSSTNKTASWEGR 360
QY 361 EASPGSSSQSVSPENQGLPPEKWLIGSLIFGLVFLVIGLVLLGRILISELRKRRYSRL 420
DB 361 EASPGSSSQSVSPENQGLPPEKWLIGSLIFGLVFLVIGLVLLGRILISELRKRRYSRL 420
QY 421 DYLLNGIYVDI 431
DB 421 DYLLNGIYVDI 431

Db 421 DYLINGIYVDI 431

RESULT 15
US-09-945-015-83
Sequence 83, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerdtsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Auscin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavini, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945, 015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132768A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132768A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO: 83
LENGTH: 431
TYPE: PRT
ORGANISM: Homo Sapien
US-09-945-015-83

Query Match 100.0%; Score 2211; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-179;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGGGSLTYTLVLIICFTLRLSASQNCLESDVVIDIOSSLSKGRNEPYTSIQ 60
DB 1 MFFGGGSLTYTLVLIICFTLRLSASQNCLESDVVIDIOSSLSKGRNEPYTSIQ 60
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DB 61 EDCINSCSTKNISGDKACNLMIPDRTKTAQPCNYLFFCPNEACPLKPAGLMSYRII 120
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DB 121 TDPFSLTRNLPSQELPOEDSLHGFQSAVPLAHHTDYSKPTDISWEDTISOKFGSSD 180
QY 181 HIEKLPKQDEASAOQLAYEKHSOSQSSPOEIAHLPEVVSALPATVAASPTTISA 240
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QY 241 TKRPATLLPTNASVTPSGTSQPOLATTAAPVTTVTSOPETTLISTVFTRAAATLOAMATT 300
DB 241 TKRPATLLPTNASVTPSGTSQPOLATTAAPVTTVTSOPETTLISTVFTRAAATLOAMATT 300
QY 301 AVLTTFQAPTDKSKSLPTIPTETISNLTNTGANNYPALMSNVESSTNNKTASWEER 360
DB 301 AVLTTFQAPTDKSKSLPTIPTETISNLTNTGANNYPALMSNVESSTNNKTASWEER 360
QY 361 EASPPSSQGSVPENQYGLPFEKWLIGSLFGVLFVLVGLVLRIGRIISSELRKRYSRU 420
DB 361 EASPPSSQGSVPENQYGLPFEKWLIGSLFGVLFVLVGLVLRIGRIISSELRKRYSRU 420
QY 421 DYLINGIYVDI 431
DB 421 DYLINGIYVDI 431

Db 421 DYLINGIYVDI 431

Search completed: April 28, 2004, 13:01:26
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2004, 12:55:48 ; Search time 21 Seconds
(without alignments)
1974.217 Million cell updates/sec

Title: US-10-677-471-83

Perfect score: 2211

Sequence: 1 MFPGGSGSLVTYLVICFLT.....LRRKRSRLDYINGIYVDI 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	155.5	7.0	770	2 T22808	hypothetical prote
4	154.5	7.0	851	2 T22696	hypothetical prote
5	154	7.0	534	2 T33903	serine-rich protei
6	151.5	6.9	1251	2 T21389	hypothetical prote
7	150.5	6.8	797	1 VGBEX1	glycoprotein X pre
8	150.5	6.8	860	2 UC4566	chitinase (EC 3.2.
9	149.5	6.8	3020	2 A43932	mucin 2 precursor,
10	149.5	6.8	3570	2 T45025	mucin MUC5B, trach
11	147.5	6.7	790	2 T34293	hypothetical prote
12	147.5	6.7	1609	2 S25345	probable membrane
13	147	6.6	662	2 A45155	mucin FIM-C.1 - Af
14	146	6.6	786	1 A47547	serine proteinase
15	144.5	6.5	505	2 B46629	mucin 6, gastric (
16	144.5	6.5	1104	2 S59310	probable membrane
17	143	6.5	626	2 S53871	Pmel 17 protein -
18	142.5	6.4	377	2 A48018	mucin 7 precursor,
19	142.5	6.4	491	2 A49179	melanoma antigen h
20	142.5	6.4	866	2 T45462	membrane glycoprot
21	141.5	6.4	867	2 T45463	membrane glycoprot
22	141.5	6.4	1161	2 S57180	probable membrane
23	141	6.4	1777	2 T34369	hypothetical prote
24	140	6.3	292	2 S24169	mucin - rat
25	140	6.3	1275	2 T33369	hypothetical prote
26	138	6.2	909	1 QRXDL2	LDL receptor 2 pre
27	137.5	6.2	1630	2 A53577	ascites stialoglyco
28	137	6.2	528	2 I47141	gastric mucin (C10
29	136.5	6.2	1229	2 T25697	hypothetical prote

30	136	6.2	503	2 S63257	probable membrane
31	136	6.2	796	2 T21460	hypothetical prote
32	135.5	6.1	322	2 A53715	apomucin precursor
33	135.5	6.1	543	2 S35047	mucin J1L7 - human
34	135.5	6.1	1299	2 T47182	hypothetical prote
35	135.5	6.1	2271	2 F90073	hypothetical prote
36	134	6.1	164	2 I53641	mucin 5AC - human
37	133.5	6.0	708	2 T19474	hypothetical prote
38	133.5	6.0	3507	2 T34513	hypothetical prote
39	133	6.0	556	2 S51892	probable membrane
40	133	6.0	610	2 S35049	mucin JER57 - huma
41	133	6.0	636	2 S63131	probable membrane
42	133	6.0	1075	2 S48992	floculation prote
43	133	6.0	1367	2 S51959	hypothetical prote
44	132	6.0	1162	2 JH0557	exo-alpha-sialidas
45	131	5.9	725	2 A41258	a-agglutinin core

ALIGNMENTS

RESULT 1

T29634
hypothetical protein C12D12.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T29634
R:Rhan, M.; Hawkins, J.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid C12D12.
A:Reference number: Z20656
A:Accession: T29634
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-825 <NHA>
A:Cross-references: EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C12D12.1
A:Experimental source: strain Bristol N2; clone C12D12
A:Genetics:
A:Gene: CESP:C12D12.1
A:Map position: X
A:Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1
C:Superfamily: Epstein-Barr virus membrane antigen gp350

Query Match	7.9%	Score 174.5;	DB 2;	Length 825;
Best Local Similarity	23.7%	Pred. No. 0.00051;		
Matches	93;	Conservative	40;	Mismatches 144; Indels 115; Gaps 17;
QY	52	NEPVYTSIOED-----CINSCCTNIGDKACNLMIPDTRK-----		88
DB	363	NTFFFTFRANDTIEIYCTVLSGSSITIDGVK---IQIDTKVQVKVDISYIYFVNTIAN		419
QY	89	-----TARQPCYIFPC-----PNEBACLPK--AKGLMSY---RIIDF		123
DB	420	PCYHOISLKQCGSVAFYVGNKLYSGYEGGANKPTVLAAPTTPGPFPYVTVVSTWS		479
QY	124	PSLTNNLSQQLPQSDLSLHGFSQAVTPPLAHNHDYSKPTDISMRDTLSOKFGSDHLE		183
DB	480	PRTTVVPTTPPPVP-----TTNTPPPAPPT--APPTVG---TSKQNTTSPHLS		526
QY	184	KLFKMDKDEASQDLAVYKEG-----HSQSSQSSDOELAHLLPENVSALPTAVVASPH		236
DB	527	TITGSIVSTPTMAQOTASPTTTPHTTASPTTTKPV--VTNSVSPSTGTTVPVP-		583
QY	237	TTSATPKPATLPLPTNASVTPSGTSPQALATTAAPVTVTSQPTTLISVFTRAAATLQA		296
DB	584	TTTGSPTTQTAPVTKPTVPSSSTTQ-----TAPVPTTSPQPPVTTSLTLTTPTVPV		638
QY	297	MAF-----TAVLTTPQA-----PTDSKSGSLFTIPT		323
DB	639	TTTVVPSSATVPTTPTTVTAATTSKAPVVTTSPTLAPISPTKLPTSPSPVGTSP-T		697
QY	324	EISNLTNTGNVYNPTALSMNSVESSTMNKTA		355

Db 698 APANLTTPTTAPVNPFT--SSTTAPTAAPVNPPTS 727

RESULT 2

553362

muscin 5AC (clone JER47) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 08-Oct-1999

C:Accession: S53362; S71065

R:Guyonnet-Duperrat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Gallegue-Biochem. J. 305, 211-219, 1995

A:Title: Characterization of the human muscin gene MUC5AC: a consensus cysteine-rich domain

A:Reference number: S53361; MUID:95126907; PMID:7826332

A:Accession: S53362

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-477 <GVY>

A:Cross-references: EMBL:234277

R:Porchet, N.

submitted to the EMBL Data Library, June 1994

A:Reference number: S71065

A:Accession: S71065

A:Molecule type: mRNA

A:Residues: 1-211,'S',213-224,'AR',227-259,'S',261-477 <POR>

A:Cross-references: EMBL:234277; NID:9563374; PIDN:CAA84031.1; PID:9563375

A:Experimental source: clone JER47

C:Genetics:

A:Gene: GDB:MUC5AC

A:Cross-references: GDB:454136; OMIM:158373

A:Map position: 11p15.5-11p15.5

C:Keywords: glycoprotein; tandem repeat

Query Match 7.3%; Score 160.5; DB 2; Length 477;

Best Local Similarity 23.8%; Pred. No. 0.0022;

Matches 76; Conservative 41; Mismatches 117; Indels 85; Gaps 13;

QY 147 SQAVPLAHHTDYKPDISW-----RDTLSQKFGSSDHL---EKLFXKD--- 189

Db 15 SQPVTRDCHLRCTWTKMFVDFPSPGPHGDKETYNINIRSEKICRPREBITRLQCRAE 74

QY 190 ---EASAOULAY-----KEKG-----HGSQSQFSS--DEIHLPLPENVALPATVAAS 234

Db 75 SHPEVSIHELQGVOCSSREGVLVCRNQDQGFKKCLNEVAVLCCERPKGCPV---ST 131

QY 235 PHTTATPKPATLILPTNAS-----VTPSGTSPQALTTAPVTTTTSOPPTLI 283

Db 132 PVTASTBEGRAISPTGSSSMQKRTTLVTTSTTSTSTSTSTSTSTSTSTSTSTST 191

QY 284 STVFRAAATLQAMATTAVALTTTFOAPTDSKGSLET-----IPTEISNLT 330

Db 192 SAPTTSTSTPQTSISSAPTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 250

QY 331 NGNGVNNPTALMSNVE-----SSTMNKTSMGREGASP-----GSSSQSVEN 375

Db 251 TTSTTSAPTST 310

QY 376 QYGLP-----FEKW 384

Db 311 THSQPVTRDCHRCRTWTKW 329

RESULT 3

722808

hypothetical protein F56H9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22808

R:Buton, J.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19618

A:Accession: T22808

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-770 <WIL>

A:Cross-references: EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F56H9.1

A:Experimental source: clone F56H9

C:Genetics:

A:Gene: CESP:F56H9.1

A:Map position: 5

A:introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Query Match 7.0%; Score 155.5; DB 2; Length 770;

Best Local Similarity 32.7%; Pred. No. 0.009;

Matches 48; Conservative 16; Mismatches 64; Indels 19; Gaps 5;

QY 219 LPENVSALPATVAASPHHTSATPKPATLILPTNASVT-----PGTSQPOLATTAPV-- 271

Db 93 VPPTTSTTTTTV--PPTTSTTTTTPPTTSSTTTTPPTTSSTTTTPPTT 150

QY 272 --TTVTSOPPTTLISTVTRAAATLQAMATTAVALTTTFOAPTDSKGSLETIPTEISNLT 329

Db 151 TSTTTTVPPTTSTTTTTPVPA--TSTAATTTVPPTTSTTTTTPPTTSTTT 205

QY 330 LNTGNVNPALMSNVSSTMNKTAS 356

Db 206 TTT---VPPTTSSTTTTLPTTT 229

RESULT 4

722696

hypothetical protein F5B11.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22696

R:Ainscough, R.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z19601

A:Accession: T22696

A:Status: preliminary; translated from GB/EMBL/DBJ

C:Genetics:

A:Gene: CESP:F5B11.3

A:Map position: 4

A:introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3

Query Match 7.0%; Score 154.5; DB 2; Length 851;

Best Local Similarity 26.6%; Pred. No. 0.012;

Matches 47; Conservative 26; Mismatches 89; Indels 15; Gaps 4;

QY 219 LPENVSALPATVAAS-----PHTTSATPKPATLILPTNASVTPSGTSQPOLATTAPV 272

Db 377 VPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTT 436

QY 273 TTVTSOPPTTLISTVTRAAATLQAMA--TTAVLTTFQAPDTS--KGSLETIPTEIS- 326

Db 437 TTVPTTTTSTTTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 496

QY 327 ---NLNTGNVNPALMSNVSSTMNKTASBGRASGSSQSVENQGLP 380

Db 497 PTTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 553

RESULT 5

739903

serine-rich protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Nov-2000

C:Accession: T39903

R:Layne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z21889

A:Accession: T39903

Db 209 TTAAATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTAATTTGSGS 267

RESULT 8

UC4566
chitinase (EC 3.2.1.14) 2 precursor - Coccidioides immitis
N.Alternate names: chitin hydrolase homolog; CT5 protein
C.Species: Coccidioides immitis
C.Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
Accession: UC4566
R.Pishko, E.J.; Kirkland, T.N.; Cole, G.T.
Gene 167, 173-177, 1995
Article: Isolation and characterization of two chitinase-encoding genes (ctsl, cts2) from
A.Reference number: UC4565; MUID:96144270; PMID:8565773
A.Accession: UC4566
A.Molecule type: mRNA
A.Residues: 1-860 <PIS>
A.Cross-references: GB:L41662
C.Genetics:
A.Gene: ct52
A.Introns: 35/3; 181/2
C.Keywords: glycoprotein; glucosidase; hydrolase; polysaccharide degradation
F.1-22/Domain: signal sequence #status predicted <SIG>
F.22-239/Domain: catalytic #status predicted <CAT>
F.23-860/Product: chitinase 2 #status predicted <MAT>
F.346-682/Region: serine/threonine-rich
F.687-860/Region: cysteine-rich
F.90.657/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 6.8%; Score 150.5; DB 2; Length 860;
Blast Local Similarity 23.9%; Pred. NO. 0.022;
Matched 78; Conservative 49; Mismatches 141; Indels 59; Gaps 12;

Db 65 NSCCSTKN-ISGDKACNLMIPTRTKTARQ---PNCLPFCCNEBACPLKPAKGLMSYRII 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
235 NPSCKAKMVMTPKSVTVTVDWVVKIRKSNPLAKLI----- 273

Qy 121 TDPSPLTRNNLPSCQ--LPEDSLHGFPSQAV-TPLAHHTDYSKPDISRDTLSQ--K 175
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
274 -----GLPKASKAALKEDYLTPGEBAKTIYSTMAKYPSYFGGM--MVMEATASEVNKK 323

Db 176 FGSSHL-----EKLKMD---EASAQLAYKEKGSSQSOSDEIAHLPEVNSALPA 228
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
324 LGLPLADIMKEVLLRCDDPPTSTVTSTTSASTSTQTSOSTMETXKTLASASTPPSSPS 383

Qy 229 TVAAVASPHTTSATPRPATLLPTNASVTPSGTSQPOLATTAAPVTVTTSQPTTLISTVFT 288
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
384 TVSPBSTMTGTSTGSTSIETVYTRSQEPSTTISTRASSTEVYTRTSQSEPSTTIS---T 440

Qy 289 RAAA----TLQAMATTAVLTTFQAPTDSKGSLEITPTEISNLTNTGNVYNFPALSMS 344
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
441 RSASTETVYTRTSQEPSTTISTWSASTETSTSSQSPSTTISTKSAPTG-----TVYTRS 495

Db 345 NVESSTMNKTKASWEGRASPGSSSGS 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
496 QDLPTTISTRSPTETETATTKSGS 522

RESULT 9

A43932
mucin 2 precursor, intestinal - human (fragments)
N.Alternate names: mucin SMUC-41
C.Species: Homo sapiens (man)
C.Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
Accession: A43963; A45106; B45106; A43932; B33332; A61257; P00328; P00329
R.Gum Jr., J.R.; Hickey, J.W.; Toribara, N.W.; Siddiki, B.; Klm, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
Article: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the
A.Reference number: A49963; MUID:94132002; PMID:8300571
A.Accession: A49963
A.Molecule type: mRNA
A.Residues: 1-639 <GUI>
A.Cross-references: GB:L21998

R.Gun J.T., J.R.Hicks, J.W.; Tortibara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S.
J Biol. Chem. 267, 13375-13383, 1992
A>Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstr
A.Reference number: A45106; PMID:93016075; PMID:1400449
A.Accession: A45106
A>Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 626-1895 <GU3>
A.Cross-references: GB:M94331, NID:g186395, PIDN:AA59163.1, PID:g186396
A>Note: sequence extracted from NCBI backbone (NCBIP:116706)
A.Accession: B45106
A>Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 2037-3020 <GU3>
A.Cross-references: GB:M94332, NID:g186397, PIDN:AA59164.1, PID:g186398
A.Experimental source: colon
A.Note: sequence extracted from NCBI backbone (NCBIP:116698)
R.Tortibara, N.W.; Gun Jr., J.R.; Cullane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.M.
J. Clin. Invest. 88, 1005-1013, 1991
A>Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorp
A.Reference number: A43932, PMID:91358717, PMID:1885763
A.Accession: A43932
A.Molecule type: DNA
A.Residues: 1343-1350, 'L', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
A.Cross-references: GB:M4027, NID:g188863, PIDN:AAA3334.1, PID:g188864
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R.Gun, J.R.; Byrd, J.C.; Hicks, J.W.; Tortibara, N.W.; Lampert, D.T.A.; Kim, Y.S.
J. Biol. Chem. 266, 6480-6487, 1991
A>Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden
A.Reference number: A33532, PMID:89197956; PMID:2703501
A.Accession: B33532
A.Molecule type: mRNA
A.Residues: 1916-2193 <GU4>
A.Cross-references: GB:M22405, NID:g188873, PIDN:AAA3334.1, PID:g188874
A.Experimental source: intestine
R.Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Baebaum, C.B.
J. Clin. Invest. 87, 77-82, 1991
A>Title: Human bronchus and intestine express the same mucin gene.
A.Reference number: A61257, PMID:91066481, PMID:1985113
A.Accession: A61257
A>Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 'T', 1925-1948, 'TTT', 1952-1954 <JAN>
A.Experimental source: bronchus
R.Xu, G.; Huan, L.; Kharri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forester,
Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A>Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t
A.Reference number: PQ0328, PMID:92198477; PMID:1550588
A.Accession: PQ0328
A.Molecule type: mRNA
A.Residues: 2328-2468 <XUG>
A.Cross-references: GB:M86523
A.Experimental source: small intestine
A.Accession: PQ0329
A.Molecule type: protein
A.Residues: 2328-2342, 'K', 2344-2354 <XUG>
C.Genetics:
A.Gene: GDB:MUC2
A.Cross-references: GDB:120203, OMIM:158370
A.Map position: 11p15.5-11p15.5
C.Subfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
C.Keywords: glycoprotein; intestine; tandem repeat
F:2766-2834/Domain: von Willebrand factor type C repeat homology <WVC>

Query Match 6.8% Score 149.5; DB 2; Length 3020;
Best Local Similarity 34.1% Pred. No. 0.13;
Matches 43; Conservative 12; Mismatches 52; Indels 19; Gaps 4;

220 PENVASLPATVAVSPHTSTATPKPAFL--LPTNASVTPL--SGTSQOLATAPPVTVT 275
+ :
1511 PASSTLTPPTTSPPTTSPPTTSPPTTSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 1570

Db	246	SHASSTHHEVTPSTTNVTPKTSR----	DTSTPYHTTSANSSRPPIITTHSSPTRS	301
Qy	288	TRAAATLOMATTAVALTTTFOAPTDSKSL	ET-IPTEISNLTLNTGNVYNPTALMSNV	346
Db	302	SPLSSTGPMATISIKTTTYPHPQTTLTHV	PPFTSSVTPSTHVIITPHAMST-	360
Qy	347	ESSTWNTASWEGREASPGSSQGSVP		373
Db	361	-----SASIHSTPTGTVP		373

Search completed: April 28, 2004, 12:59:51
Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2004, 12:54:37 ; Search time 17 Seconds
(without alignments)
1320.132 Million cell updates/sec

Title: US-10-677-471-83
Perfect score: 2211
Sequence: 1 MFEGGSGSLTYTLVILICFLT.....LRRKRYSLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151.5	6.9	1240	1 Y0U3 CAEEL	Q09550 caenorhabd
2	150.5	6.8	797	1 VGUX HSEVB	P28968 equine hepr
3	150.5	6.8	860	1 CHIZ COCPO	P54197 coccidioid
4	149.5	6.8	5179	1 MUCC HUMAN	Q02817 homo sapien
5	149.5	6.8	5703	1 MUSB HUMAN	Q9H844 homo sapien
6	148.5	6.7	1233	1 MUSA HUMAN	P98088 homo sapien
7	147.5	6.7	1609	1 FIIG YEAST	P25653 saccharomyc
8	147	6.6	662	1 MUCI XENLA	Q05049 xenopus lae
9	146	6.6	786	1 STUB DROME	Q05319 drosophila
10	144.5	6.5	1140	1 YM96 YEAST	Q04893 saccharomyc
11	143	6.5	626	1 PM17 MOUSE	Q06596 mus musculu
12	142.5	6.4	491	1 PM17 BOVIN	Q06154 bos taurus
13	142	6.4	397	1 SEPL MOUSE	Q62170 mus musculu
14	141.5	6.4	1161	1 DANA YEAST	P47179 saccharomyc
15	136	6.2	503	1 WSC2 YEAST	P53832 saccharomyc
16	136	6.2	799	1 ZXDB HUMAN	P98168 homo sapien
17	136	6.2	3178	1 YS89 CAEEL	Q09624 caenorhabd
18	135	6.1	803	1 ZXDB HUMAN	P98169 homo sapien
19	133	6.0	556	1 WSC3 YEAST	Q12215 saccharomyc
20	133	6.0	636	1 YNRE YEAST	P53882 saccharomyc
21	133	6.0	1075	1 FLOS YEAST	P33894 saccharomyc
22	132	6.0	1162	1 TCNA TRYCR	P23253 trypanosoma
23	131	5.9	725	1 AGAL YEAST	P32323 saccharomyc
24	130.5	5.9	524	1 P60 LISIV	Q01837 listeria iv
25	129.5	5.9	400	1 AMYH YEAST	P10667 xenopus lae
26	129.5	5.9	1367	1 VGP8 EBV	P03324 Epstein-bar
27	128.5	5.8	510	1 CX56 CHICK	P29415 gallus galli
28	128	5.8	605	1 WSC4 YEAST	P38739 saccharomyc
29	128	5.8	870	1 SYPL YEAST	P25663 saccharomyc
30	127.5	5.8	559	1 CAFE HUMAN	Q13112 homo sapien
31	127.5	5.8	634	1 HWP1 CANAL	P46593 candida alb
32	127.5	5.8	634	1 HWP1 CANAL	P46593 candida alb
33	127	5.7	1322	1 YAG3 YEAST	P39712 saccharomyc

34	126.5	5.7	1260	1 A1S1 CANAL	P46590 candida alb
35	126	5.7	405	1 SDC3 CHICK	P26261 gallus galli
36	125.5	5.7	909	1 LDI1 XENLA	Q99087 xenopus lae
37	125	5.7	600	1 SP96 DICDI	P14328 dictyostell
38	124.5	5.6	1306	1 MSB2 YEAST	P32334 saccharomyc
39	124	5.6	1374	1 YMN3 YEAST	Q03099 saccharomyc
40	124	5.6	1513	1 MDC2 RAT	Q62635 rattus norv
41	124	5.6	1681	1 YRF2 YEAST	P49105 saccharomyc
42	124	5.6	1859	1 YRF3 YEAST	P53345 saccharomyc
43	124	5.6	1859	1 YRF6 YEAST	P53819 saccharomyc
44	123.5	5.6	503	1 PDX1 MOUSE	Q970M4 mus musculu
45	123.5	5.6	544	1 GP10 DICDI	Q06885 dictyostell

ALIGNMENTS

RESULT 1	ID	Y0U3 CAEEL	STANDARD	PRT	1240 AA.
AC	009550				
DT	01-NOV-1995 (rel. 32, Created)				
DT	10-OCT-2003 (rel. 42, Last sequence update)				
DT	10-OCT-2003 (rel. 42, Last annotation update)				
DE	Hypothetical protein F26C11.3 in chromosome II.				
GN	F26C11.3.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
OX	Rhabditidae; Pelodierinae; Caenorhabditis.				
NCBI_Taxid=6239;					
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Bristol N2;				
RA	Matthews P.;				
RL	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	REVISIONS.				
RA	Dubin R.;				
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: Contains 1 Sushi (SCR) domain.				
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CC	or send an email to license@isb-sib.ch .				
DR	EMBL; Z47072; CAA87369.2; -				
DR	PIR; T21389; T21389.				
DR	WormPep; F26C11.3; CE32880.				
DR	InterPro; IPR000436; Sushi_SCR_CCP.				
DR	Pfam; PF00084; sushi_1.				
DR	SMART; SM00032; CCP; 1.				
KW	Hypothetical protein.				
FT	DOMAIN 207 1183				
SQ	SEQUENCE 1240 AA; 132292 MW; AAC1421B2ESD922EB CRC64;				
Query Match	6.9%; Score 151.5; DB 1; Length 1240;				
Best Local Similarity	22.4%; Pred. No. 0.024;				
Matches	93; Conservative 46; Mismatches 161; Indels 115; Gaps 17;				
QY	17 CELTRLASQNCLEKSLKEDVVIDIQSLSKIRGNEPVTSTQBDCT-----64				
DB	82 CQCVLTSSSTETGTYKFLDREFFRVSSAEIASTTSLPTTISPSLNCVWLSPPNSFSEWI 141				
QY	65 -----NSCGSTKNI-----SGDKACNLMIFPDKTARQPNCY--LFFC-PNEEACP 107				
DB	142 DKGQTNLRNNGCCGSETSIQVNLSSDS--TRWILTTSQSWNVANLIMLYCTPN--ACP 197				
QY	108 LKPAKGLMSYRITITPPSLT-----RNLPSQELPQSDSLHGFQSAVTPFLAHHHDVSKP 163				

Db 198 QOSMNTNCSNISTSSSTMLSSTLTLETETREBSSTGS-TQTTPTSTPTTTTTP 256
QY 164 TDISWRDLTSQKFGSSDHLKLFKMEDEASQALLAYKEKHSOSSQSFSDOEIAHLLENV 223
Db 257 ME-----QSSIVSS----- 265
QY 224 SALPATAVASPHHTSATPKPATLPTFNASVTPSGISQOLATTPAPVTTTSGOPTTII 283
Db 266 -----VQKRTSEDKPSSSTVPTASSTESSSTSP-MAETSSSTSSQSSPAST-- 314
QY 284 STVFTRAAATLOAMATTAV--LTTTFQAPLDSKGLFTIPFTEINLTNTNGVNPATL 341
Db 315 STV--PESITVSGTPTTGLTTSTINEQSTSSGGHSTFTTSE-TPETSTDFTAST 371
QY 342 S-----MSNVESSTMNKTASWEGREASPGSSSQSVPENQGLPF--EKMLL 386
Db 372 SSSSDSTQSSNAQSTIENGSTTNTNFTSAPSTSSRPATPTTNTMPCGTMMML 426

RESULT 2

VGIX_HSVB STANDARD; PRT; 797 AA.
AC P28968;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Glycoprotein X precursor.
GN 71.
OS Equine herpesvirus type 1 (strain Abap) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirinae.
OX NCBI_TaxID=31520;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1";
RL Virology 189:304-316(1992).
CC -----
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CC -----
DR EMBL; M86664; AA02506.1; -.
DR PIR; H36802; VGBEX1.
DR InterPro; IPR007110; IG-like.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 22
FT CHAIN 23 797 POTENTIAL.
FT DOMAIN 23 797 GLYCOPROTEIN X.
FT TRANSMEM 766 790 SER/THR-RICH.
FT CARBOHYD 590 590 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 797 AA; 80342 MW; 50C9ED9211F55B2 CRC64;

Query Match 6.8%; Score 150.5; DB 1; Length 797;

Best Local Similarity 24.3%; Pred. No. 0.016; Matches 131; Indels 25; Gaps 2;

Db 158 TDYSKPTDISWRDLTSQKFGSSDHLKLFKMEDEASQALLAYKEKHSOSSQSFSDOEIAH 217
Db 29 TSSSSSTSGSGSTSSGTTNSSSPTSPPTSSSPPTSTHTSSSSSTSSSTAATSS 88
QY 218 LIPENVSAIPATAVASPHHTSATPKPATLPTFNASVTP----- 256
Db 89 SAPSTASTTSIPTSTSTETTTTTPASTTPTTTTAATTAATTAATTAATTAATTAATTA 148
QY 257 ---SSTSQOLAT-TAPVTTVTSQPTTLISTVTRAAATLOAMATTAVLTTTQAPTD 312
Db 149 ATATATSTPTTTTPTTTTATTTTATTTVPTASTTTDTTAAATTAATTAATTAATTA 208

QY 313 SKGLFTIPFTEINLTNTNGVNPATLSMNVESSTMNKTASWEGREASPGSSSQGS 371
Db 209 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 267

RESULT 3

CH12_COCOPO STANDARD; PRT; 860 AA.
ID CH12 COCPO
AC P54197;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endochitinase 2 precursor (EC 3.2.1.14).
GN CTS2.
OS Coccidioides posadasii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; mitosporic Onygenales; Coccidioides.
OX NCBI_TaxID=199306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C735;
RX MEDLINE=96144270; PubMed=8566773;
RA Pishko E.U., Kirkland T.N., Cole G.T.;
RT "Isolation and characterization of two chitinase-encoding genes
RT (cts1, cts2) from the fungus Coccidioides immitis";
RL Gene 167:173-177(1995).
CC CC
CC -1- FUNCTION: May be associated with endospore germination.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -1- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL; U41662; AA92642.1; -.
DR HSSP; P23472; 2HVM.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AB.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 860 ENDOCHITINASE 2.
FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 860 AA; 91395 MW; 5E34B54FPA663F3C CRC64;

Query Match 6.8%; Score 150.5; DB 1; Length 860;

Best Local Similarity 23.9%; Pred. No. 0.018; Matches 78; Conservative 49; Mismatches 141; Indels 59; Gaps 12;

QY 65 NSCSTKN-IGDRACNIMTDRKTARQ---PNCYLFPCNEACPLKPAKGLMSYRII 120
Db 235 NPSCSAKRWVNPXSVTYTVDVWKYIRKSGNPLAKFI----- 273
QY 121 TDPSLTNRLPSQE--LPQEDSLHGOFSQAV-TPLAHHTDYSKPTDISWRDLTSQ--K 175
Db 274 -----GLPASASAANKEDYLTPEAKTKVSTYMAKYSTPFGM--MVEEATASENNK 323
QY 176 FGSSDHL-----EKLKMD---EASQALLAYKEKHSOSSQSFSDOEIAHLLENVSAIPA 228
Db 324 LGGYPADIMKEVLLRCDDPDPPTSTVSTASTSGSTMETKTLASATTPSPSS 383
QY 229 TVAAVSPHTSATPKPATLPTFNASVTPSGISQOLATTAATTAATTAATTAATTAATTA 288
Db 384 TVSPBSTWQITSTGSTSIETVTRTSQEPPTTITSTRASSTPVTTRSGEPSTTIS--T 440


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FT CARBOHYD 4373 4373 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4422 4422 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4438 4438 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4502 4502 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4616 4616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4627 4627 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4752 4752 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4787 4787 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4881 4881 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4888 4888 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4955 4955 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 4970 4970 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 5019 5019 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 5038 5038 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 5069 5069 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CONFLICT 1351 1351 H -> L (IN REF. 3)
FT CONFLICT 1412 1412 T -> S (IN REF. 3)
FT CONFLICT 1449 1449 L -> P (IN REF. 3)
FT CONFLICT 1504 1504 M -> T (IN REF. 3)
FT CONFLICT 1504 1504 G -> S (IN REF. 2)
SQ SEQUENCE 5179 AA, 540295 MW, 85CD07571FB9A5663 CRC64;

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Query Match 6.8%; Score 149.5; DB 1; Length 5179;
Best Local Similarity 34.1%; Pred. No. 0.2;
Matches 43; Conservative 12; Mismatches 52; Indels 19; Gaps 4;

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OY 220 PENVALPATVAVASPHHTSATPKPATL-LPTNASVFP--SGTSOPQLATAPPTVT 275
DB 1511 PASTTLPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 1570
OY 276 SQPPTTLIS-----TVFTRAAATLQAMTAVLTTFQAPDSCSLPTTPT 323
DB 1571 TTPPTTSPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 1627
OY 324 EISNLT 329
DB 1628 PPTSTT 1633

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RESULT 5

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MUSB_HUMAN STANDARD; PRT; 5703 AA.
AC Q9H84; O00447; O00573; O14985; O15494; O95291; O95451; O14881;
AC Q99552; Q9UE28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mucin 5B precursor (Mucin 5 subtype B, tracheobronchial) (High
DE molecular weight salivary mucin MG1) (Sublingual gland mucin).
GN MUSCB OR MUC5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OK NCBI_taxonomy606;
RN [1]
RP SEQUENCE OF 1-1594 FROM N.A.
RA Chen Y., Di Y.P., Wu R.;
RT "Molecular cloning of the amino-terminal and 5'-flanking region of the
RT human MUC5B mucin gene.";
RN [2]
RP Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-1325 FROM N.A.
RX MEDLINE=9900274; PubMed=9790959;
RA Offner G.D., Nunes D.P., Keates A.C., Afchal N.H., Troxler R.F.;
RT "The amino-terminal sequence of MUC5B contains conserved
RT multifunctional D domains: implications for tissue-specific mucin
RT functions.";
RN [4]
RP Biochem. Biophys. Res. Commun. 251:350-355(1998).
RN [5]
RP SEQUENCE OF 40-1324 FROM N.A.
RX MEDLINE=99023932; PubMed=9804771;
RA Desseyn J.-L., Bulsine M.P., Porchet N., Aubert J.-P., Laine A.;
RT "Genomic organization of the human mucin gene MUC5B: cDNA and genomic

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RT sequences upstream of the large central exon.";
RL J. Biol. Chem. 273:30157-30164(1998).
RN [4]
RP SEQUENCE OF 1326-4895 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=9716151; PubMed=9013550;
RA Desseyn J.-L., Guyonnet-Duperrat V., Porchet N., Aubert J.-P.,
RA Laine A.;
RT "Human mucin gene MUC5B, the 10.7 kb large central exon encodes
RT various alternate subdomains resulting in a super-repeat. Structural
RT evidence for a 11p15.5 gene family.";
RN [5]
RP J. Biol. Chem. 272:3166-3178(1997).
RN [6]
RP SEQUENCE OF 4057-4480 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=97292540; PubMed=9147051;
RA Nielsen P.A., Bennett E.P., Wandall H.H., Therkildsen M.H.,
RA Hannibal J., Clausen H.;
RT "Identification of a major human high molecular weight salivary mucin
RT (MG1) as tracheobronchial mucin MUC5B.";
RL Glycobiology 7:413-419(1997).
RN [6]
RP SEQUENCE OF 4721-5703 FROM N.A.
RC TISSUE=Gall bladder;
RX MEDLINE=97293229; PubMed=9164870;
RA Keates A.C., Nunes D.P., Afchal N.H., Troxler R.F., Offner G.D.;
RT "Molecular cloning of a major human gall bladder mucin: complete C-
RT terminal sequence and genomic organization of MUC5B.";
RN [7]
RP Biochem. J. 324:295-303(1997).
RN [7]
RP SEQUENCE OF 4809-5687 FROM N.A.
RC TISSUE=Sublingual gland;
RX MEDLINE=96125355; PubMed=8554565;
RA Troxler R.F., Offner G.D., Zhang F., Ioncheva I., Oppenheim F.G.;
RT "Molecular cloning of a novel high molecular weight mucin (MG1)
RT from human sublingual gland.";
RL Biochem. Biophys. Res. Commun. 217:1112-1119(1995).
RN [8]
RP SEQUENCE OF 4859-5703 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97347489; PubMed=9201995;
RA Desseyn J.-L., Aubert J.-P., Porchet N., Laine A.;
RT "Genomic organization of the 3 region of the human MUC5B mucin.";
RN [8]
RP J. Biol. Chem. 272:16873-16883(1997).
CC -1- FUNCTION: Salivary mucin that is thought to contribute to the
CC lubricating and viscoelastic properties of whole saliva.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed mainly in bronchus glands and also
CC in submaxillary glands, endocervix, gall bladder, and pancreas.
CC -1- PTM: Highly glycosylated.
CC -1- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
CC -1- SIMILARITY: Contains 3 WFRC domains.
CC -1- SIMILARITY: Contains 4 WFRC domains.
CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
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CC -----
DR EMBL, AF107890; AAC33673.1; -
DR EMBL, AF086604; AAC67545.1; -
DR EMBL, AJ004862; CAA06167.1; -
DR EMBL, Z72496; CAA96577.1; -
DR EMBL, X74955; CAA52910.1; -
DR EMBL, U61836; AAB61398.1; -
DR EMBL, U78554; AAC51344.1; -
DR EMBL, U78552; AAC51344.1; JOINED.
DR EMBL, U78553; AAC51344.1; JOINED.
DR EMBL, U78551; AAC51343.1; -

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RL J. Biol. Chem. 269:12933-12939(1994).
 RN [3]
 RP SEQUENCE OF 153-1233 FROM N.A.
 RC TISSUE=Placenta, and Trachea;
 RX MEDLINE=98285541; PubMed=9620876;
 RA Buisine M.P., Desseyn J.L., Porchet N., Degand P., Laine A.,
 RA Aubert J.-P.;
 RT "Genomic organization of the 3'-region of the human MUC5AC mucin gene:
 RT additional evidence for a common ancestral gene for the 11p15.5 mucin
 RT gene family.";
 RL Biochem. J. 332:729-738(1998).
 RN [4]
 RN SEQUENCE OF 284-1233 FROM N.A.
 RP MEDLINE=95293957; PubMed=7775418;
 RX Loeffleuer T., Roche F., Hill A.S., Lacasa M., Fox M., Swallow D.M.,
 RA Zwielsbaum A., Real F.X.;
 RT "Characterisation of a mucin cDNA clone isolated from HT-29 mucus
 RT secreting cells: The 3' end of MUC5AC";
 RL J. Biol. Chem. 270:13665-13673(1995).
 CC -1- FUNCTION: MAJOR AIRWAY GLYCOPROTEIN.
 CC -1- SUBUNIT: Multimeric.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: TRACHEOBRONCHIAL MUCOSAE (NOT SOLELY).
 CC -1- SIMILARITY: TO VARIOUS MUCINS.
 CC -1- SIMILARITY: Contains 1 VWFc domain.
 CC -1- SIMILARITY: Contains 1 VWFd domain.
 CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
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 CC -----
 DR EMBL; AJ298319; CAC83676.1; -
 DR EMBL; U06711; AA18431.1; -
 DR EMBL; AJ001402; CA04737.1; -
 DR EMBL; AJ001403; CA04738.1; -
 DR EMBL; Z48314; CAA8307.1; -
 DR Genew; HGNC:7515; MUC5AC.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO; GO:0007155; P:cell adhesion; NAS.
 DR InterPro; IPR006208; Cys_knot.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR002919; TIL_Cystrich.
 DR InterPro; IPR001007; VWF_C.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF00007; Cys_knot; 1.
 DR Pfam; PF00093; Vwf; 1.
 DR Pfam; PF00094; Vwf; 1.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS0208; VWFc_1; 2.
 DR PROSITE; PS0184; VWFc_2; 2.
 DR Repeat; Glycoprotein.
 KW NON_TER
 FT 1
 FT DOMAIN 431 496 VWFc 1.
 FT DOMAIN 500 659 VWFd.
 FT DOMAIN 688 712 5 X 5 AA TANDEM REPEATS OF T-T-V-G-P/S.
 FT REPEAT 688 692 1.
 FT REPEAT 693 697 2.
 FT REPEAT 703 702 3.
 FT REPEAT 708 712 4.
 FT REPEAT 712 712 5.
 FT DOMAIN 857 923 VWFc 2.
 FT DOMAIN 962 1026 VWFc 3.
 FT DOMAIN 1111 1199 CTCK.
 FT DISULFID 1111 1161 BY SIMILARITY.
 FT DISULFID 1136 1175 BY SIMILARITY.
 FT DISULFID 1140 1191 BY SIMILARITY.
 FT DISULFID 1158 1193 BY SIMILARITY.

[illegible]

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DR EMBL: X59720; CAA4254.1; -
 DR PIR: S25345; S25345.
 DR Geronline: 138986; -
 DR SGD: S0000685; FIG2.
 DR GO: GO:0009277; C:cell wall (sensu Fungi); IDA.
 DR GO: GO:0000753; P:cellular morphogenesis during conjugation w. .; IMP.
 DR GO: GO:0000755; P:cycogamy; IMP.
 DR SEQUENCE 1609 AA; 16604 MW; 7D6AD7F85A7B852 CRC64;

Query Match 6.7%; Score 147.5; DB 1; Length 1609;
 Best Local Similarity 22.4%; Pred. No. 0.061;
 Matches 88; Conservative 63; Mismatches 164; Indels 77; Gaps 14;

QY 41 IGSLSKGRGNEPVYTSQEDCINSCCTKNISGDKACNMFDR---KTARQNCY 96
 DB 1057 IMSSSNVISTNEKBSSTSPYNFSSGSLPSSSTPSQYSLSTATTINGIKTV-----Y 1111
 QY 97 LFFCNEEACPKPAKGLMSYRIITDFPSLTRNLPSOBLPOBDSILHGFQSOAVPLAH 156
 DB 1112 TWCPLAEKSTV--AASSQSSSVDRFVSSK--PSSLSQ--TSQYTLSTRTTISGL 1165
 QY 157 HTDYKSPKPIDISWRDILSQKFGSSDHLKFKMDEASQALLAYKXGHSQSSQ-----F 209
 DB 1166 KIVYTTWCLPSTKSLTGATGTTSTPAKVRITSASATSTISLSTESSESSGYLSKV 1225
 QY 210 SSDQELHLLPENVALPATVAVASP-----HTSATPKPAT---LTPNNAV 254
 DB 1226 CGGTCTQDVPFQ--SSSPASTLAYSPSVSTSSSSPSTTTASTLTSTHTSVPLPSSSI 1284
 QY 255 TFSGTSGPQPLATT---APVTVTSQPPFTLLISTVTRAAATLQMA-----TTAVLT 304
 DB 1285 SASSPSSTSLSTSLSPSPAFSTSTLPTATAVSSSTIASLSPSSKSLSPVSSSILM 1344
 QY 305 TTFQAPDTSKGSLETTIPTEISNLTNTGNYNPT----- 339
 DB 1345 SQFSSSSSSSSSLASLPSTLISP-TVDTVSVLQPTSTIATLCTDSQCQEVSTICNGSN 1403
 QY 340 ---ALSMNVESSTANKTASMEGREASPGSSS 368
 DB 1404 CDVVTSTATTPPSTVDTWTCTGSECOKTTSS 1435

RESULT 8
 MUC1_XENLA STANDARD; PRT; 662 AA.
 ID MUC1_XENLA
 AC Q05049;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integumentary mucin C.1 (FIM-C.1) (Fragment).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 OC NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 7).
 RC TISSUE=Skin;
 RX MEDLINE=93077556; PubMed=1447205;
 RA Hauser F., Hoffmann W.;
 RT "P-domains as shuffled cysteine-rich modules in integumentary mucin
 RT C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic
 RT polymorphism.";
 RL J. Biol. Chem. 267:24620-24624(1992).
 CC -I- FUNCTION: Could be involved in defense against microbial

CC infections. Protects the epithelia from external environment.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=7;
 CC Comment=Additional isoforms seem to exist. Experimental
 CC confirmation may be lacking for some isoforms;
 CC Name=1;
 CC IsoId=Q05049-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q05049-2; Sequence=VSP_004650;
 CC Name=3;
 CC IsoId=Q05049-3; Sequence=VSP_004651;
 CC Name=4;
 CC IsoId=Q05049-4; Sequence=VSP_004647, VSP_004648;
 CC Name=5;
 CC IsoId=Q05049-5; Sequence=VSP_004646, VSP_004649, VSP_004650;
 CC Name=6;
 CC IsoId=Q05049-6; Sequence=VSP_004646, VSP_004648;
 CC Name=7;
 CC IsoId=Q05049-7; Sequence=VSP_004647;
 CC -I- TISSUE SPECIFICITY: Skin.
 CC -I- PTM: Extensively O-glycosylated.
 CC -I- SIMILARITY: Contains 6 p-type (trefoil) domains.
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 CC or send an email to license@isb-sib.ch).

DR EMBL: 102115; AAA74725.1; -
 DR PIR: A45155; A45155.
 DR HSSP: P01359; 2PSP.
 DR InterPro: IPR000519; P_trefoil.
 DR Pfam: PF00088; trefoil; 6.
 DR PRINTS: PR00680; PTFREFOIL.
 DR SMART: SM00018; PD; 6.
 DR PROSITE: PS00025; P_TREFOIL; 6.
 KW Repeat; Glycoprotein; Alternative splicing.
 FT NON TER 1
 FT DOMAIN 81 144
 FT REPEAT 81 88
 FT REPEAT 89 96
 FT REPEAT 97 104
 FT REPEAT 105 112
 FT REPEAT 113 120
 FT REPEAT 121 128
 FT REPEAT 129 136
 FT REPEAT 137 144
 FT DOMAIN 161 202
 FT REPEAT 161 202
 FT REPEAT 218 301
 FT REPEAT 218 224
 FT REPEAT 225 239
 FT REPEAT 240 249
 FT REPEAT 250 259
 FT REPEAT 260 275
 FT REPEAT 276 287
 FT REPEAT 288 294
 FT REPEAT 295 301
 FT DOMAIN 306 347
 FT DOMAIN 353 394
 FT DOMAIN 402 522
 FT REPEAT 402 411
 FT REPEAT 412 419
 FT REPEAT 420 431
 FT REPEAT 432 443
 FT REPEAT 444 453
 FT REPEAT 454 460
 FT REPEAT 461 472
 FT 8 X 8 AA APPROXIMATE TANDEM REPEATS,
 ALA/THR-RICH.
 FT 1-1.
 FT 1-2.
 FT 1-3.
 FT 1-4.
 FT 1-5.
 FT 1-6.
 FT 1-7.
 FT 1-8.
 FT P-TYPE 1.
 FT 8 X APPROXIMATE TANDEM REPEATS, THR-RICH.
 FT 2-1.
 FT 2-2.
 FT 2-3.
 FT 2-4.
 FT 2-5.
 FT 2-6.
 FT 2-7.
 FT 2-8.
 FT P-TYPE 2.
 FT P-TYPE 3.
 FT 12 X APPROXIMATE TANDEM REPEATS, THR-RICH.
 FT 3-1.
 FT 3-2.
 FT 3-3.
 FT 3-4.
 FT 3-5.
 FT 3-6.
 FT 3-7.

```

FT REPEAT 473 479 3-8.
FT REPEAT 480 491 3-9.
FT REPEAT 492 498 3-10.
FT REPEAT 499 515 3-11.
FT REPEAT 516 522 3-12.
FT DOMAIN 525 566 P-TYPE 4.
FT DOMAIN 572 613 P-TYPE 5.
FT DOMAIN 620 661 P-TYPE 6.
FT DISULFID 162 188 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT DISULFID 182 199 BY SIMILARITY.
FT DISULFID 307 333 BY SIMILARITY.
FT DISULFID 317 332 BY SIMILARITY.
FT DISULFID 327 344 BY SIMILARITY.
FT DISULFID 354 380 BY SIMILARITY.
FT DISULFID 374 391 BY SIMILARITY.
FT DISULFID 526 552 BY SIMILARITY.
FT DISULFID 536 551 BY SIMILARITY.
FT DISULFID 546 563 BY SIMILARITY.
FT DISULFID 573 599 BY SIMILARITY.
FT DISULFID 583 598 BY SIMILARITY.
FT DISULFID 593 610 BY SIMILARITY.
FT DISULFID 621 647 BY SIMILARITY.
FT DISULFID 631 646 BY SIMILARITY.
FT DISULFID 651 658 BY SIMILARITY.
FT VARSPLC 240 259 Missing (in isoform 5 and isoform 6).
FT VARSPLC 250 259 /FTId=VSP_004646.
FT VARSPLC 276 294 Missing (in isoform 4 and isoform 7).
FT VARSPLC 278 278 Missing (in isoform 4 and isoform 6).
FT VARSPLC 278 278 /FTId=VSP_004648.
FT VARSPLC 278 278 Missing (in isoform 5).
FT VARSPLC 306 350 /FTId=VSP_004649.
FT VARSPLC 420 498 /FTId=VSP_004650.
FT VARSPLC 420 498 Missing (in isoform 3).
FT VARSPLC 420 498 /FTId=VSP_004651.
FT VARIANT 276 276 K -> E.
FT VARIANT 354 354 C -> R.
FT VARIANT 415 415 T -> A.
SQ SEQUENCE 662 AA; 67774 MW; F085277F1ED2FD40 CRC64;

Query Match 6.6%; Score 147; DB 1; Length 662;
Best Local Similarity 26.9%; Pred.No.0.022;
Matches 49; Conservative 19; Mismatches 78; Indels 36; Gaps 5;

QY 228 ATVAASHTTSATKPKATLLEPTNASVTPSGISQQLATAPVTT-----VTSQPP 279
DB 394 STSQVAATKKT--TPTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPT 451
QY 280 TLLISTVFTRAATLOAMATTAVALTTTFOAPTDSKSLFTTFTETISNLTNTGNVNP 339
DB 452 TTTPTTTTATTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPT 506
QY 340 ALSMSNVSSSTNKTKAS-----WEGREASPGSSSGQSVENQ---YG 378
DB 507 TTTTPTTTTATTTTTSGECKMEPSKADCGYPGITESGCRKGCPCFDSIQTWKCFYS 566
QY 379 LP 380
DB 567 LP 568

RESULT 9
STUB_DROME STANDARD; PRT; 786 AA.
AC Q05319;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Serine proteinase stubble (EC 3.4.21.-) (Stubble-scubblويد protein).
GN SB OR SB-SBD.

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=93281671; PubMed=7685111;
RA Appel L.F., Prot M., Abu-Shumay R., Hammonds A., Garbe J.C.,
RT Fristrom D., Fristrom J.;
RT "The Drosophila Stubble-scubblويد gene encodes an apparent
transmembrane serine protease required for epithelial
morphogenesis."
RT Proc. Natl. Acad. Sci. U.S.A. 90:4937-4941(1993).
CC -! FUNCTION: Hormone dependent protease required for epithelial
morphogenesis. Has a dual function, detaches imaginal disc cells
from extracellular matrices through its extracellular proteolytic
domain and transmits an outside-to-inside signal to its
intracellular domain to modify the cytoskeleton during
morphogenesis. May be able to activate itself.
CC -! SUBCELLULAR LOCATION: Type II membrane protein.
CC -! INDUCTION: By 20-hydroxyecdysone (20HE).
CC -! SIMILARITY: Belongs to peptidase family S1.
CC -! CAUTION: It is uncertain whether Met-1 or Met-24 is the initiator.
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CC
DR EMBL; L11451; AAA8918.1; -.
DR PIR; A47547; A47547.
DR HSRP; P00763; IDPO.
DR MEROPS; S01.225; -.
DR FLYBase; FBgn0003319; Sb.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IMP.
DR InterPro; IPR009603; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Transmembrane; Glycoprotein; Zymogen;
KW Signal-anchor.
FT CHAIN 1 542 NON-CATALYTIC CHAIN (POTENTIAL).
FT CHAIN 543 786 CATALYTIC CHAIN (POTENTIAL).
FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 80 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 81 786 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 543 786 SERINE PROTEASE.
FT DOMAIN 267 276 POLY-SER.
FT DOMAIN 287 298 POLY-GLN.
FT DOMAIN 391 478 SER/THR-RICH.
FT DOMAIN 412 422 POLY-THR.
FT DOMAIN 471 478 POLY-SER.
FT ACT_SITE 589 589 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 639 639 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 737 737 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 531 659 INTERCHAIN (BY SIMILARITY).
FT DISULFID 574 590 BY SIMILARITY.
FT DISULFID 703 722 BY SIMILARITY.
FT DISULFID 733 762 BY SIMILARITY.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 786 AA; 85010 MW; CE3E755760BDE4D CRC64;

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QY 317 LETIPTEISNLTNTG---NYNPTALSMNSVESSTMNKTASWEGREASPGSSQSGSVP 373
 Db 231 TREVSTERSGTTVQGTTPELVETTAGVSTPEPAGSN-TSSFMTEGTASLS--PLP 287

QY 374 ENQYGLPFEX 383
 Db 288 DDTATLVLEK 297

RESULT 13
 SEPL_MOUSE STANDARD; PRT; 397 AA.

AC 062170;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P-selectin glycoprotein ligand 1 precursor (PSGL-1) (selectin P ligand).
 DE SELPLG OR SELPL OR SELPL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/C;
 MEDLINE=96220265; PubMed=8639776;
 RA Yang J., Galipeau J., Kozak C., Furie B.C., Furie B.;
 RT "Mouse P-selectin glycoprotein ligand-1: molecular cloning, chromosomal localization, and expression of a functional P-selectin receptor."
 RT Blood 87:4176-4186 (1996).
 RL Blood 87:4176-4186 (1996).
 CC -1- FUNCTION: Binds to P-, E- and L-selectins. The calcium-dependent high affinity interaction with P-selectin mediates the tethering and rolling of neutrophils and T-lymphocytes on endothelial cells.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: Highly O-glycosylated. Also N-glycosylated (By similarity).
 CC -1- PTM: Sulfated in the N-terminal region; sulfation is necessary for P-selectin binding (By similarity).
 CC -----
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 CC -----
 CC EMBL, X91144; CAA62583.1; -.
 DR MGD; MGI:106689; Selpl.
 KW Cell adhesion; Glycoprotein; Transmembrane; Signal; Repeat; Sulfation.

FT SIGNAL 1 17
 FT PROPEP 18 41
 FT CHAIN 42 397
 FT DOMAIN 18 307
 FT TRANSMEM 308 328
 FT DOMAIN 329 397
 FT DOMSWIC 397
 FT MOD RES 54 54
 FT MOD RES 56 56
 FT CARBOHYD 66 66
 FT CAROCHD 261 261
 FT DOMAIN 126 225
 FT SWIMIN 126 135
 FT REPEAT 126 135
 FT REPEAT 136 145
 FT REPEAT 146 155
 FT REPEAT 156 165
 FT REPEAT 156 175
 FT REPEAT 176 185
 FT REPEAT 186 195
 FT REPEAT 196 205

FT REPEAT 206 215 9.
 FT REPEAT 216 225 10.
 SQ SEQUENCE 397 AA; 41781 MW; 512B645FEB21E4B2 CRC64;
 Query Match 6.4%; Score 142; DB 1; Length 397;
 Best Local Similarity 25.4%; Pred. No. 0.024;
 Matches 80; Conservative 46; Mismatches 129; Indels 60; Gaps 16;

QY 117 YRIITDFSLTRNLS-----QELP-----QEDSLMLGQFQGAUTPLAHHTDYSKPRD 165
 Db 54 YTYNTDPELLKNVTNTVAAPHELPTTVMLERDSTAGTSERATEKIA--TTDPLAP-- 109
 QY 166 ISWRDTLSQFGSSSHLEKLFMDASAOILAAYKKGSSQSGSFSDDEIAHLLENVSA 225
 Db 110 -----GTGGTANGMLSTDSATQWSLTSVTQVPASFEVTSQP-AMMEFTSQP 157
 QY 226 LPATVAVASPHITSA-TPKPATLLPTNLSV-----TPSGTSQP---QIATTPAP-PVTYVT 275
 Db 158 APMEAFSTQPAPEADTSKPA---PTEAFSTKPAPEAFSTQPAPEADTSKPAPEAFST 214
 QY 276 SQP-PTTLISVYPTTAATLQAMATTAVLTTFQAPTSKGLPTIPTEISNLTNTG--F 334
 Db 215 SKPAPTEAETQLPR---IQAVKTLFTTSATEVSPTEPTMETAS--TESNESTIFLGP 269
 QY 335 VYNPTALSMNSVESSTMNKTASWEGREASPGSSQSGSVENQYGLPFEXKHLIGSL--F 392
 Db 270 -----SVTHLPDGLKK-----GLIYTPGNSPAPPTLPSSDLIPVQCLLIILIASL 317

QY 393 GYLFLVIGLVILGRT 407
 Db 318 ATIFLVCTVLAVAL 332

RESULT 14
 DAN4 YEAST STANDARD; PRT; 1161 AA.

AC P47179;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cell wall protein DAN4 precursor.
 GN DAN4 OR YJR151C OR J2223.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Scarcez T.;
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP REGULATION.
 RX MEDLINE=21113168; PubMed=11160904;
 RA Cohen B.D., Serfil O., Abromova N.E., Davies K.J., Lowry C.V.;
 RT "Induction and repression of DAN1 and the family of anaerobic mannoprotein genes in Saccharomyces cerevisiae occurs through a complex array of regulatory sites."
 RT Nucleic Acids Res. 29:799-808 (2001).
 CC -1- FUNCTION: Component of the cell wall (By similarity).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).
 CC -1- PTM: Extensively O-glycosylated (Potential).
 CC -1- SIMILARITY: Belongs to the SRP1 / T1P1 family.
 CC -----
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 CC -----
 CC EMBL, Z49651; CAA89684.1; -.

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DR PIR; S57180; S57180.
DR Germonline; 141984; -.
DR SGP; S0003912; DAM4.
DR GO; GO:0009277; C:cell wall (eenu Fungl); IDA.
DR InterPro; IPR000992; SRP1_TiPl.
DR Pfam; PF00660; SRP1_TiPl; 1.
DR PROSITE; PS00724; SRP1_TiPl; 1.
DR Cell wall; Glycoprotein; Membrane; GPI-anchor; signal; Lipoprotein.
KW SIGNAL.
FT CHAIN 1 24
FT PROPEP 1147 1146 CELL WALL PROTEIN DAM.
FT LIPID 1146 1146 REMOVED IN MATURE FORM (POTENTIAL).
FT GPI-anchor amidated asparagine
FT (potential).
SQ SEQUENCE 1161 AA; 118358 MW; 7954C15D6F0CA58 CRC64;

Query Match 6.4%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 25.8%; Pred. No. 0.1; Mismatches 97; Indels 45; Gaps 11;
Matches 60; Conservative 31;

QY 155 HHHTDYSKPTDISMDTLISQKFGSSDHLKLT--FKMDEASQQLA---YKEKSHSQSSQF 209
DB 57 NHHKETPTSEIA-----AAVPDYGDPFTRRLGISGDEVTRMTGVPMVSTRKPAISIA 111
QY 210 SSGDEIAHLPL-----ENVSALEPATVAVASPHHTSATPKPATLLPTNASVTPSGTS 260
DB 112 LSKGDIYVAIPSTSTSTTKSSTSTPTTITSTSTSTSTSTSTSTSTSTSTSTSTSTST 166
QY 261 QPOLATTAPEVTTSQPTTLISTVFTRAAATLQAMATTAVALTTTFOAPTDSKGLSTETI 320
DB 167 -----TSTPTTSTSTSTPTT--ST--TSTPTTSTSTSTPTTSTSTSTPTTSTST--TT 215
QY 321 PTEISNLTNTGNVYNPTALSMNSVSESTMNKTAWEGRASPGSSSGSGSV 373
DB 216 PTTSTSTSTPTTST--TPT-----TSTSTSTQSTSTKSTTPTTSSSTSTP 258

RESULT 15
WSC2_YEAST STANDARD; PRT; 503 AA.
AC P53832;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Cell wall integrity and stress response component 2 precursor.
GN WSC2 OR YNL283C OR N0583.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OK NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Messenguy F.; Dubois E.; Vlierendeels F.; Scherens B.; Pierard A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 WSC domain.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; 271559; CAA96195.1; -.
DR PIR; S63257; S63257.
DR Germonline; 143289; -.
DR SGP; S0005227; WSC2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IGI.
DR GO; GO:0007047; P:cell wall organization and biogenesis; IGI.
DR GO; GO:0009408; P:response to heat; IGI.
DR GO; GO:0007266; P:rho protein signal transduction; IGI.

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DR InterPro; IPR002889; WSC.
DR Pfam; PF01822; WSC; 1.
DR SMART; SM00321; WSC; 1.
KW Cell wall; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 23
FT CHAIN 24 503
FT TRANSMEM 326 346
FT DOMAIN 121 319
FT CARBOHYD 394 394 SER/THR-RICH.
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 503 AA; 52292 MW; F2392A73C5CBAB50 CRC64;

Query Match 6.2%; Score 136; DB 1; Length 503;
Best Local Similarity 27.2%; Pred. No. 0.082; Mismatches 110; Indels 2; Gaps 2;
Matches 55; Conservative 35;

QY 204 SSSQFSSDDEIAHLPEENVGALPATVAVASPHHTSATPKPA-TLPTNASVTPSGTSQP 262
DB 137 SSSSTSVSSKISTKLDITKSTSSATSSSSSTSTSTSSSETTSSSSSSSSSTST 196
QY 263 QLATTAPEVTTSQPTTLISTVFTRAAATLQAMATTAVALTTTFOAPTDSKGLSTETI 322
DB 197 STSTSTSTSTSSPSSTSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSST 255
QY 323 TEISNLTNTGNVYNPTALSMNSVSESTMNKTAWEGRASPGSSSGSGSV 362
DB 256 TSIQSTHYTRVYVTSVSGANQASTIFTRTSVYAVVSTSSSTSSSLNKGSSSSKS 315
QY 383 KMLIGSLFGLVFLVIGLVLL 404
DB 316 KGLSGAIGAVGVGVCSTVAL 337

```

Search completed: April 28, 2004, 12:58:20
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2004, 12:55:12 ; Search time 45 Seconds
(without alignments)
3021.963 Million cell updates/sec

Title: US-10-677-471-83

Perfect score: 2211

Sequence: 1 MFPGEGSLTYTLVLCFLT.....LRRKRSRLDYINGIYVDI 431

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	431	4 Q9H8J5	Q9H8J5 homo sapien
2	2210	100.0	431	4 Q8NEC1	Q8NEC1 homo sapien
3	2039	92.2	431	6 Q95XG7	Q95XG7 macaca fasc
4	2022	91.5	397	4 Q9NM60	Q9NM60 homo sapien
5	1179.5	53.3	414	11 Q8OV71	Q8OV71 mus musculu
6	1164.5	52.7	414	11 Q8CR33	Q8CR33 mus musculu
7	503	22.7	194	11 Q8K010	Q8K010 mus musculu
8	197.5	8.9	392	11 Q8VCP2	Q8VCP2 mus musculu
9	197	8.9	449	4 Q9H2K4	Q9H2K4 homo sapien
10	196.5	8.9	392	11 Q9DBN1	Q9DBN1 mus musculu
11	188	8.5	449	4 Q96F05	Q96F05 homo sapien
12	180.5	8.2	1349	4 Q8WMQ4	Q8WMQ4 homo sapien
13	168	7.6	519	5 Q7YTR7	Q7YTR7 caenorhabd
14	160.5	7.3	477	5 Q14887	Q14887 homo sapien
15	157.5	7.1	2448	4 Q8WMQ5	Q8WMQ5 homo sapien
16	156.5	7.1	328	4 Q00446	Q00446 homo sapien

17	155.5	7.0	769	5 Q17921	Q17921 caenorhabd
18	155.5	7.0	770	5 Q20908	Q20908 caenorhabd
19	154	7.0	534	3 Q94317	Q94317 schizosacch
20	152	6.9	744	3 Q8TRG9	Q8TRG9 schizosacch
21	150.5	6.8	382	5 Q9XZ28	Q9XZ28 litomosoid
22	147.5	6.7	790	5 Q20599	Q20599 caenorhabd
23	147.5	6.7	842	5 Q95QF5	Q95QF5 caenorhabd
24	146	6.6	316	12 Q8VOM4	Q8VOM4 equine herp
25	146	6.6	457	5 Q86AK1	Q86AK1 dictyostell
26	145.5	6.6	629	5 Q24017	Q24017 drosophila
27	145.5	6.6	716	4 Q9NYE4	Q9NYE4 homo sapien
28	145	6.6	1079	5 Q9N4S7	Q9N4S7 caenorhabd
29	144.5	6.5	377	4 Q8YAX7	Q8YAX7 homo sapien
30	144.5	6.5	505	4 Q14395	Q14395 homo sapien
31	144.5	6.5	683	5 Q8BRH5	Q8BRH5 drosophila
32	144.5	6.5	787	5 Q9VEY6	Q9VEY6 drosophila
33	144	6.5	22152	4 Q8WXT7	Q8WXT7 homo sapien
34	143.5	6.5	1414	11 Q80Z22	Q80Z22 mus musculu
35	143.5	6.5	2850	11 Q8V0L5	Q8V0L5 equine herp
36	142.5	6.4	826	12 Q8V0L5	Q8V0L5 equine herp
37	142.5	6.4	866	12 Q39782	Q39782 equine herp
38	142.5	6.4	867	12 Q39782	Q39782 equine herp
39	142.5	6.4	1444	5 Q9VTN2	Q9VTN2 drosophila
40	142.5	6.4	1514	5 Q8SY55	Q8SY55 drosophila
41	142	6.4	483	5 Q9W4M2	Q9W4M2 drosophila
42	142	6.4	873	5 Q9W468	Q9W468 drosophila
43	141.5	6.4	1391	13 Q7ZM07	Q7ZM07 brachydanio
44	141	6.4	374	12 Q8V0L6	Q8V0L6 equine herp
45	141	6.4	626	11 Q9CZB2	Q9CZB2 mus musculu

ALIGNMENTS

RESULT 1	Q9H8J5	PRELIMINARY:	PRT:	431 AA.
AC	Q9H8J5			
DT	01-MAR-2001 (TREMBL)	16, Created		
DT	01-MAR-2001 (TREMBL)	16, Last sequence update		
DT	01-OCT-2002 (TREMBL)	22, Last annotation update		
DE	Hypothetical protein FLJ13560.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Isoagi T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,			
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,			
RA	Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,			
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuo Y.,			
RA	Ninomiya K., Iwayanagi T.,			
RT	"NEO human cDNA sequencing project."			
RL	Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK023622; BAB14621.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 431 AA; 46810 MW; 1691364160F089AE CRC64;			
Query Match	100.0%; Score 2211; DB 4; Length 431;			
Best Local Similarity	100.0%; Pred. No. 8.2e-159;			
Matches	431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

Qy	1 MFPGEGSLTYTLVLCFLTRLASQWCKKSLIEDVVIDIOSSISKGRNEPYSTQ 60	
Db	1 MFPGEGSLTYTLVLCFLTRLASQWCKKSLIEDVVIDIOSSISKGRNEPYSTQ 60	
Qy	61 EDCINSCSTNNISGDKACNIMIFDTRKTAOPNCYLFPCNENACPLKPAKGLMSYRII 120	
Db	61 EDCINSCSTNNISGDKACNIMIFDTRKTAOPNCYLFPCNENACPLKPAKGLMSYRII 120	

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QY 121 TDFPSLTNRNLPQSELPOEDSLHGFQSOAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
Db 121 TDFPSLTNRNLPQSELPOEDSLHGFQSOAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
QY 181 HLEKLFKMDKASAOQLAYKEKGHSOSSQSSDOEIAHLHPENVASLPATVAASPHTTSA 240
Db 181 HLEKLFKMDKASAOQLAYKEKGHSOSSQSSDOEIAHLHPENVASLPATVAASPHTTSA 240
QY 241 TPKPATLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLOAMATT 300
Db 241 TPKPATLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLOAMATT 300
QY 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360
Db 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360
QY 361 EASPSGSSQGVSPENQYGLPPEKMLLIGSLFGVLFLVIGLGRILSESLRRKRY SRL 420
Db 361 EASPSGSSQGVSPENQYGLPPEKMLLIGSLFGVLFLVIGLGRILSESLRRKRY SRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

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RESULT 2

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QY 09NEC1 PRELIMINARY; PRT; 431 AA.
AC 09NEC1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein FLJ10298.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Struhsberg R.;
DR EMBL; BC032998; AAH32998.1; -.
KW Hypothetical protein.
SQ SEQUENCE 431 AA; 46824 MW; 1BCEBD168AC939D CRC64;

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Query Match 100.0%; Score 2210; DB 4; Length 431;
 Best Local Similarity 99.8%; Pred. No. 9, 7e-159;
 Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MFFGEGSLTYTLVLIICFLTRLASQNCCLKSLIEDVVIDIOSLSKIGRNEPVYTSQ 60
Db 1 MFFGEGSLTYTLVLIICFLTRLASQNCCLKSLIEDVVIDIOSLSKIGRNEPVYTSQ 60
QY 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCYLFPCNEBACPLKPAKGLMSYRII 120
Db 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCYLFPCNEBACPLKPAKGLMSYRII 120
QY 121 TDFPSLTNRNLPQSELPOEDSLHGFQSOAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
Db 121 TDFPSLTNRNLPQSELPOEDSLHGFQSOAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
QY 181 HLEKLFKMDKASAOQLAYKEKGHSOSSQSSDOEIAHLHPENVASLPATVAASPHTTSA 240
Db 181 HLEKLFKMDKASAOQLAYKEKGHSOSSQSSDOEIAHLHPENVASLPATVAASPHTTSA 240
QY 241 TPKPATLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLOAMATT 300
Db 241 TPKPATLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLOAMATT 300
QY 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360
Db 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360

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Db 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360
QY 361 EASPSGSSQGVSPENQYGLPPEKMLLIGSLFGVLFLVIGLGRILSESLRRKRY SRL 420
Db 361 EASPSGSSQGVSPENQYGLPPEKMLLIGSLFGVLFLVIGLGRILSESLRRKRY SRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

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RESULT 3

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QY 09SKG7 PRELIMINARY; PRT; 431 AA.
AC 09SKG7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Temporal cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Ieeki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB060888; BAB46892.1; -.
KW Hypothetical protein.
SQ SEQUENCE 431 AA; 47104 MW; BFI0996887F76C69 CRC64;

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Query Match 92.2%; Score 2039; DB 6; Length 431;
 Best Local Similarity 92.3%; Pred. No. 8, 1e-146;
 Matches 398; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

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QY 1 MFFGEGSLTYTLVLIICFLTRLASQNCCLKSLIEDVVIDIOSLSKIGRNEPVYTSQ 60
Db 1 MFFGEGSLTYTLVLIICFLTRLASQNCCLKSLIEDVVIDIOSLSKIGRNEPVYTSQ 60
QY 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCYLFPCNEBACPLKPAKGLMSYRII 120
Db 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCYLFPCNEBACPLKPAKGLMSYRII 120
QY 121 TDFPSLTNRNLPQSELPOEDSLHGFQSOAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
Db 121 TDFPSLTNRNLPQSELPOEDSLHGFQSOAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
QY 181 HLEKLFKMDKASAOQLAYKEKGHSOSSQSSDOEIAHLHPENVASLPATVAASPHTTSA 240
Db 181 HLEKLFKMDKASAOQLAYKEKGHSOSSQSSDOEIAHLHPENVASLPATVAASPHTTSA 240
QY 241 TPKPATLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLOAMATT 300
Db 241 TPKPATLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLOAMATT 300
QY 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360
Db 301 AVLTTPQAPTDKSGSLFTIPFTEISNLTNTGAVNPTALSMNSVSSSTNKTASWEGR 360
QY 361 EASPSGSSQGVSPENQYGLPPEKMLLIGSLFGVLFLVIGLGRILSESLRRKRY SRL 420
Db 361 EASPSGSSQGVSPENQYGLPPEKMLLIGSLFGVLFLVIGLGRILSESLRRKRY SRL 420
QY 421 DYLINGIYVDI 431
Db 421 DYLINGIYVDI 431

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RESULT 4
Q9NM60 PRELIMINARY: PRT: 397 AA.
ID Q9NM60:
AC Q9NM60:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ10298.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagasuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Nimomiya K., Iwayanagi T.;
RT "NEBO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK001160; BAA91526.1;
KW Hypothetical protein.
SQ SEQUENCE 397 AA; 43062 MW; E2FEFF2E61122C62 CRC64;

Query Match 91.5%; Score 2022; DB 4; Length 397;
Best Local Similarity 92.1%; Pred. No. 1.4e-144;
Matches 397; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MFPGEGSLTYTLVLTICFLTLRLSASQNLKSLSDVVIDIQSSLKGRGNEPYTSTQ 60
DB 1 MFPGEGSLTYTL-----GIRGNEPYTSTQ 26

QY 61 EDCINSCSTKNISGDKACNLMIPDRTKAROPNCYLFPCPNBEACPLKPAKGLMSYRII 120
DB 27 EDCINSCSTKNISGDKACNLMIPDRTKAROPNCYLFPCPNBEACPLKPAKGLMSYRII 86

QY 121 TDFPSLTNLPSQELPQEDSLHGFQSOAVTPPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
DB 87 TDFPSLTNLPSQELPQEDSLHGFQSOAVTPPLAHHHTDYSKPTDISWRDTLSQKFGSSD 146

QY 181 HLEKLFKMDKDEASQQLLAYKEKGHSOSQSSPOEIAHLIPENVSAIPATVAASPHTTSA 240
DB 147 HLEKLFKMDKDEASQQLLAYKEKGHSOSQSSPOEIAHLIPENVSAIPATVAASPHTTSA 206

QY 241 TPKPATLLPTNASVTPSGTSPQOLATTAAPVTVTSOPEPTLLISTVFTRAAATLQAMATT 300
DB 267 TPKPATLLPTNASVTPSGTSPQOLATTAAPVTVTSOPEPTLLISTVFTRAAATLQAMATT 266

QY 301 AVLTTTFOAPDPSKSLFTIPTTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGR 360
DB 267 AVLTTTFOAPDPSKSLFTIPTTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGR 326

QY 361 EASPGSSQSGVPENQYGLPFEKMLIGSLFGVLFVIGVLLGRILISESLRRKRYSL 420
DB 327 EASPGSSQSGVPENQYGLPFEKMLIGSLFGVLFVIGVLLGRILISESLRRKRYSL 386

QY 421 DYLINGIYVDI 431
DB 387 DYLINGIYVDI 397

RESULT 5
Q80V71 PRELIMINARY: PRT: 414 AA.
ID Q80V71:
AC Q80V71:
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 9130403P13R1k protein.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.P., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaratte P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood U., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalski J., Skalski J.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Breast tumor;
RX Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC039930; AAH39930.1;
KW "Generation and initial analysis of more than 15,000 full-length human
SQ SEQUENCE 414 AA; 44531 MW; 84AFB759D1B22755 CRC64;

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Query Match 53.3%; Score 1179.5; DB 11; Length 414;
Best Local Similarity 60.3%; Pred. No. 6.5e-81;
Matches 260; Conservative 36; Mismatches 118; Indels 17; Gaps 6;

QY 1 MFPGEGSLTYTLVLTICFLTLRLSASQNLKSLSDVVIDIQSSLKGRGNEPYTSTQ 60
DB 1 MLFRGT-SLAVALVVISFLTPRSSAGQNLTKSLSDVVIDIQSSLKGRGNEPYHATQ 59

QY 61 EDCINSCSTKNISGDKACNLMIPDRTKAROPNCYLFPCPNBEACPLKPAKGLMSYRII 120
DB 60 EDCVAGCCSTYDIADGDKACNLMIPDRTKAROPNCYLFPCPNBEACPLKPAKGLMSYRII 119

QY 121 TDFPSLTNLPSQELPQEDSLHGFQSOAVTPPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
DB 120 RDFPLTSANSSLOQTQESILLDHSPGATPGRPRTAGYKRPGLSLMSDGSLSKSTAPL 179

QY 181 HLEKLFKMDKDEASQQLLAYKEKGHSOSQSSPOEIAHLIPENVSAIPATVAASPHTTSA 240
DB 180 HLEKLFKMDKDEASQQLLAYKEKGHSOSQSSPOEIAHLIPENVSAIPATVAASPHTTSA 237

QY 241 TPKPATLLPTNASVTPSGTSPQOLATTAAPVTVTSOPEPTLLISTVFTRAAATLQAMATT 300
DB 238 TPKPATLLPTNASVTPSGTSPQOLATTAAPVTVTSOPEPTLLISTVFTRAAATLQAMATT 289

QY 301 AVLTTTFOAPDPSKSLFTIPTTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGR 360
DB 290 AVLTTTFOAPDPSKSLFTIPTTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGR 343

QY 361 EASPGSSQSGVPENQYGLPFEKMLIGSLFGVLFVIGVLLGRILISESLRRKRYSL 420
DB 344 RVSVGSASLNGKPSQHGSLPFEKMLIGTLGVLFLVIGVLLGRILISESLRRKRYSL 403

QY 421 DYLINGIYVDI 431
DB 404 DYLINGIYVDI 414

RESULT 6

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Q9CR33 PRELIMINARY; PRT; 414 AA.
 ID Q9CR33;
 AC Q9CR33;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE 9130403P13Rik protein (weakly similar to NTRM100115 protein).
 GN 9130403P13Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kaebawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Mateno Y., Nikaido I., Pesole G., Quackenbush J.,
 Schramm L.M., Struhl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Botelli D., Boujunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gaston-Pich S., Hall J.D., Hofmann M., Hume D.B., Kamuya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Saeki H., Sato K., Scheenbach C., Seta T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Welter C., Whiteaker C., Wilming L.,
 Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
 Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon, and Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA THE FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK018660; BAB31329.1; -
 DR EMBL; AK018635; BAB31319.1; -
 DR EMBL; AK033526; BAC28341.1; -
 DR EMBL; AK033557; BAC28357.1; -
 DR EMBL; AK046837; BAC32892.1; -
 DR MGI; MGI:1914979; 9130403P13Rik.
 SQ SEQUENCE 414 AA; 44822 MW; 29BB9197C916BA8E CRC64;
 Query Match 52.7%; Score 1164.5; DB 11; Length 414;
 Best Local Similarity 59.9%; Pred. No. 8.9e-80;
 Matches 258; Conservative 37; Mismatches 119; Indels 17; Gaps 6;
 QY 1 MFFGEGSLTYTLVLTICFTLRLSASONCLKSLSDVYDIQSSJSGKGRNEPVYGTQ 60
 DB 1 MLFRCST-SLAVSLVLSFLTRPSSAGONCLTSLSDVYDIQSSJSGKGRNEPVHATQ 59
 QY 61 EDCINSCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
 DB 60 EDCIACCCSTKDIADGKACNLMIFDTRKTDRQPNCYLFFCPNEEACPLKPAKGLVYRLI 119
 QY 121 TDFPFLTNLPBQELPQBDLSLHGQFQAVPLAHNHDYKPTDISMRDTSQKFGSSD 180
 DB 120 RDPFLTSANSSIQQLTQGEFFLLDHSFQATGFTTPRAGYPRPTLSMSDRSLSTAPL 179
 QY 181 HLEKLFKMDKDEASQQLAVYKEKSHSQSSQFSDPQIAHLPEKVNALPPTVAASPHTTSA 240
 DB 180 HLRKRIKADERTSMQL--PEEKSHSQSLQLPSELKVAHLPLKTVPTTPVAVAPLRNVSA 237

QY 241 TPKPATLPTNASTVPSTSQPOLATTAPPTVYTSQPEPTTLISTVFPRAATLQAMATT 300
 DB 238 TLKPELLT-TSISVYAKTLKQKE-ATTASPVTVTSKLPVGVSGTSFT-----PVYHQ 289
 QY 301 AVLTTPPAQPDPSGSLTETIPFTEISNLTLTGAVNVPNTALSMNVESSTNNKTASMEGR 360
 DB 290 AALNTTFOAHTDSKGLTFMPFGGSLT-----SDPRHKSSTSESSITNNKTASMEGR 343
 QY 361 EASPGSSQGSVPENQYGLPEFKWLLIGSLFGLVFLVIGLVLLGRILSESLRRKYSRL 420
 DB 344 RVSGSASLNGKPSQSHLSFEKMLLIGTLLCGVLVIGLVLLGRMLVEALRRKYSRL 403
 QY 421 DYLINGIYVDI 431
 DB 404 DYLINGIYVDI 414
 RESULT 7
 ID Q8K010 PRELIMINARY; PRT; 194 AA.
 AC Q8K010;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Similar to hypothetical protein FLJ10298 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Straubeberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013772; AAH1372.1; -
 KW Hypothetical protein.
 FT NON-TER
 SQ SEQUENCE 194 AA; 20701 MW; 11C1F299E1FB3C44 CRC64;
 Query Match 22.7%; Score 503; DB 11; Length 194;
 Best Local Similarity 59.5%; Pred. No. 3.1e-30;
 Matches 122; Conservative 13; Mismatches 56; Indels 14; Gaps 4;
 QY 227 PATVAASPHTTSATPKPATLLPTNASTVPSTSQPOLATTAPPTVYTSQPEPTTLISTV 286
 DB 4 PTVVAAPLRNVSAATLKPALL-TSISVYAKTLKQKE-ATTASPVTVTSKLPVGVSGTS 61
 QY 287 FTRPAATLQAMATTAVLTTPPAQPDPSGSLTETIPFTEISNLTLTGAVNVPNTALSMNV 346
 DB 62 FT-----PVYTHQALNTTFOAHTDSKGLTFMPFGGSLT-----SDPRHKSST 109
 QY 347 EESTNNKTSMEGRASPGSSQGSVPENQYGLPEFKWLLIGSLFGLVFLVIGLVLLGR 406
 DB 110 EESITNNKTASMEGRASVGSASLNGKPSQSHLSFEKMLLIGTLLCGVLVIGLVLLGR 169
 QY 407 ILSESLRRKYSRLDYLINGIYVDI 431
 DB 170 MLVEALRRKYSRLDYLINGIYVDI 194
 RESULT 8
 ID Q8VCP2 PRELIMINARY; PRT; 392 AA.
 AC Q8VCP2;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE RIKEN cDNA 1810055G02 gene.
 GN 1810055G02Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Struhsberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019471; AAH19471.1; -
 MDG; MG1:1919306; 1810055G02R1K.
 SQ SEQUENCE 392 AA; 41081 MW; 1D79796C791211FA CRC64;
 Query Match 8.9%; Score 197.5; DB 11; Length 392;
 Best Local Similarity 26.5%; Pred. No. 9.3e-07;
 Matches 89; Conservative 37; Mismatches 115; Indels 95; Gaps 14;
 QY 156 HTDVSXKPTDIDWRDLSGKFGSSDHLKLFKMDASAGLLAYKEKGHSQSOF----- 209
 DB 88 HGTNSTPT-----TREGTDRV-----TSRTLAAPTSGSPSAEQTRPTTA 130
 QY 210 ----SSDOEIAHLLENVNSALPAT--VAVASPHTT-----SATPKPATLLPTN 251
 DB 131 GLPPLSTPHAEVPRTVASVSPRTAMATVAPHATLTAAGVNTSDPHRTSPSAKSTPD 190
 QY 252 -ASVTPSGISQPOLATTAPVTT-----VTSQPTTLISTVFTRAAT 293
 DB 191 TSSKXPIPTSGAQIOCTTQVLTDPVHSTAGRSALSPENATLEPTTQVOTK-EPSAST 249
 QY 294 LGAMATTAVALTTFOAPTSKSGLETPTEISNLTNTGNYNPALMSMNVESSTMK 353
 DB 250 VPARATISLSPDVVISPTTQPS--PTLP-----TQGTGG--PGTLTTEQVGTXTSG 298
 QY 354 TASWEGREASPGSSSGSV-----PENQGLPFE-----KMLIGSLIFGV 394
 DB 299 TNS-----AGPISRSSGDIKVPPTDSCPSQCGVLTVDALPLSLVNMILLVLLVGV 353
 QY 395 LFLVIGLVILGRILSRLKRYSLDYINGIYVD 430
 DB 354 TLFIAVLVAFALQAYESYKKDYQVDYLINGMYAD 389
 RESULT 9
 Q9H2K4 PRELIMINARY; PRT; 449 AA.
 ID Q9H2K4;
 AC Q9H2K4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE DM4E3.
 GN C10RF24.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21295044; PubMed=11401438;
 RA Tweils R.C.J., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H.,
 RA Hey P.J., Levy E., Nakagawa Y., Phillips M.S., Todd J.A., Hess J.F.,
 RA "The Sequence and Gene Characterization of a 400-Kb Candidate Region
 RT for IDDD4 on Chromosome 11q13."
 RL Genomics 72:231-242(2001).
 DR EMBL; AF264781; AAG3636.1; -
 DR InterPro: IPR001395; Aldc/ket red.
 DR PROSITE; PS00063; ALDOXERO_REDUCTASE_3; 1
 SQ SEQUENCE 449 AA; 46100 MW; 11C8B0FC3BBP921 CRC64;
 Query Match 8.9%; Score 197; DB 4; Length 449;
 Best Local Similarity 22.2%; Pred. No. 1.2e-06;
 Matches 117; Conservative 49; Mismatches 166; Indels 196; Gaps 18;
 QY 13 LVITCLTIRLSNQCLKSLSDVYIDIQSSLSKIRGNEPYTSTQEDCINSCSTON 72
 DB 5 LVILWIFSLSLSSHAASNDPRNFVNKKWKGLVKYNASVETVNDNTSDVYMAAAS--- 61
 QY 73 ISGDKACNIMIFTRTAQPNCYLFCFNEACPLKPAKGLMRYRIIDPSELTNLPS 132

DB 62 -----PVTLTKG-----TSAHLNS 76
 QY 133 QELPOEDSLHGOFSQAVTPLAHHRTDYSKPRDIDSWRDLGKFGSSDHLKLFKMDAS 192
 DB 77 MEVTEEDT-----SRTDVSEP-----ATSGGAADGVTSIAPTAVAS 112
 QY 199 AQLLAYKEKGHSQSOFSSDOEIAHLLENVNSALPATVAVASPHT-----TSATPKPATL 247
 DB 113 STTA-----SITTAASMTVASSAP--TTAASSTTASIAPIPTTAASMTAASSTPML 164
 QY 248 ---LPTNNAV--TPS--GTSQPOLATTAPVTTVTSQPTTLISTVFTRAATLQAMAT 300
 DB 165 ALPAPTSTSTGTPPTGTATGHPSLSLTAQAQVKSALPRTATLATLATRA-----QTVA 220
 QY 301 A-----VLTTRQAPDSDG 315
 DB 221 ANTSSPMSTRPSPSKHMSDITASVPWPMPQAGPIQSVSDQPVVNTNTKSTPMSPNT 280
 QY 316 SLETTPTTEISNLTNTGNYNPAL-----SMS-NVESSTMKKTASMEG- 359
 DB 281 TPEPAPPTV--VTYKAQAREPTLASVPVPHPTSPPEMEANSPTTQSPMPTQRAACP 338
 QY 360 -----REASPGSSSGSVPENQYG--LP-----FE 382
 DB 339 GTSQAPQEVETATGTGTSTGTPRSGCTKMPATDSCPSQCGVMTTEPLTQAVVD 398
 QY 383 KMLIGSLIFGVLFVIGLVILGRILSRLKRYSLDYINGIYVD 430
 DB 399 KTLILVLLIGVLTFLTVLVLALQAYESYKKDYQVDYLINGMYAD 446
 RESULT 10
 Q9DBN1 PRELIMINARY; PRT; 392 AA.
 ID Q9DBN1;
 AC Q9DBN1;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE 1810055G02R1K protein.
 GN 1810055G02R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.W., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladevall R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita S., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK007868; BAB25319.1; -
 DR MGD; MG1:1919306; 1810055G02R1K.
 SQ SEQUENCE 392 AA; 41095 MW; 6BBA958C73489874 CRC64;

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Query Match      8.9%; Score 196.5; DB 11; Length 392;
Best Local Similarity 26.1%; Pred. No. 1.1e-06;
Matches 88; Conservative 42; Mismatches 110; Indels 97; Gaps 15;

OY 156 HTTDSKPTDMSWRTLSQKFGSSDHLKLFKMDASAOQLAYKKGHSSQSSQFSDDEI 215
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 88 HGTNSTSTPT-----TREGTIDRV-----TSRTLAVPTSSGSSSAEOTRPTTI 129
OY 216 AHL-----LPE-NVSALPAT--VAVASPHTT-----SATEPKPATLLPT 250
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 130 AGLPELSTPHAEVPRPTNASVSPTMTAAVTVAHTTLAGVTNVSDPHTRTSPAKSKPT 189
OY 251 N-ASTPEGCTSQPOLATTAPVTT-----VTSQPPPTLLSTVTRDAA 292
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 190 DTSSKNPIPTSGAQIQGTIVQLTTDQPVHSTAGSALSPSNATLEPTTQVQTK-EPAS 248
OY 293 TLQAAATTAVLTTPQAPRTDSKSLJETTFTEISNLTLNTGNVNPPTLSMNSVSSMTN 352
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 249 TVPARATISLSPVDVVISPTTQPS--PTLP-----TQGTGG--EGTLTTEQVQTKTTS 297
OY 353 KTASWEGREASFGSSSSQGSV-----PENQYGLPFE-----KWLILGSLFLFG 393
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 298 GTAS-----AGPTSRSSGDIKVPPTDSCQPSGTQGGYLVITDALTPSLVNMKMLLVLLVG 352
OY 394 VLFLVIGLVLAGRIISGLRRKRYSLDYLINGIYVD 430
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 353 VTLFLAVLMFALQAYESYKKDYQVVDYLINGMYAD 389

RESULT 11
OY 096F05 PRELIMINARY; PRT; 449 AA.
AC 096F05;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chromosome 11 open reading frame 24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC011765; AA011765.1; -.
DR GeneW; HGNC:1174; C11orf24.
DR InterPro; IPR001395; Aldol/Kec_red.
DR PROSITE; PS00063; ALDOXETO_REDUCTASE_3; 1.
SQ SEQUENCE 449 AA; 46142 MW; BF984AA360FC415 CRC64;

Query Match      8.5%; Score 188; DB 4; Length 449;
Best Local Similarity 22.0%; Pred. No. 5.8e-06;
Matches 116; Conservative 49; Mismatches 167; Indels 196; Gaps 18;

OY 13 LVIIICFLTRLASQNCCLKSLLEDVVIDIQSSLSKIGINEPVYSTQEDCINSCSTKN 72
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 5 LVLIIIFSLISSEHSAASNDPRNFPVNMKMKGLVBRNASEVETVDKITSDDVYMAAS--- 61
OY 73 ISGDACNLMTFDTKTAQPNQCYLPCPNBEACPLKPAKGLMSYRIITDPFSLTRNIPS 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 -----PVTLTKG-----TSAAHNS 76
OY 133 CELPOEDSLHGFQFAVTRPLAHNHTDYSKPTDMSRDTLSQKFGSSDHLKLFKMDAS 192
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 77 MEVTEDT-----SRTDVSEP-----ATSGVAADSVISIAFTAVAS 112
OY 193 AQLLAYKEKGHSSQSSQFSDDEIAHLPENVASALPATVAVASPHT-----TSATPKPATL 247
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 113 STTA-----SITTAASMTVASSAP--TTAASSTVASIAPTTAASMTAASSTPMTL 164
OY 248 ---LPTNASV--TPS--GTSPQALATTAPVTTVTTSQPTTLLISTVTRAAATLOAMATT 300
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DB 165 ALPAPTSTSTGRSTTATGHPISLSTALAQPKSSALPRTATLATRA---QYVATT 220
OY 301 A-----VLTTPQAPDTSKG 315
DB 221 ANTSSPMSTRSPSKHMPSDTAASVPVPMRQAGCPISQVSDQPVNTTKSTPMBSNT 280
OY 316 SLETPTEISNLTLNTGNVNPPTAL-----SMS-NVESSTNMKTASMEG- 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 281 TPEAPPTPTV--VTTTKAQAREPTASVPVPHSTPIEMEMASPTTQSPMPYQRAAGP 338
OY 360 -----REASPGSSSQSSVPENOYG--LP-----FE 382
DB 339 GTSQAPQEVETEAPPTGDTSTGPTRRSSGCTKMPATDSCQPSGTQGYVNVVTEPLTQAVVD 398
OY 383 KWLILGSLFLGVFLVIGLVLAGRIISGLRRKRYSLDYLINGIYVD 430
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 399 KTLVLVLLGVTLEFITYLVLPALQAYESYKKDYQVVDYLINGMYAD 446

RESULT 12
OY 08WMQ4 PRELIMINARY; PRT; 1349 AA.
AC 08WMQ4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Mucin 5 (Fragment).
GN MUC5AC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21426417; PubMed=1153137;
RA Escande F., Aubert J.P., Porchet N., Buisine M.P.;
RT "Human mucin gene MUC5AC: organization of its 5'-region and central
RT repetitive region.";
RL Biochem. J. 358:763-772 (2001).
DR EMBL; AJ298318; CAC83675.1; -.
FT NON_TER 1
FT NON_TER 1349
SQ SEQUENCE 1349 AA; 135600 MW; 4DC3C1544F1EE5BA CRC64;

Query Match      8.2%; Score 180.5; DB 4; Length 1349;
Best Local Similarity 21.6%; Pred. No. 9.2e-05;
Matches 88; Conservative 62; Mismatches 174; Indels 83; Gaps 14;

OY 4 GGEGSLTYTVI-----ICFLTRLASQNCCLKSLLEDVVID-----IQSSLSKIGIRNE 53
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 517 GGDKE-TYNNIIRSGEKICRRPQETRLQ-CRAKSHPEVSIENHGGVYVQCSREBGL---- 570
OY 54 PVYISTQEDCINSCSTKNISGD-KACNLMTFDRKTAQPNQCYLPCPNBEACPLKPAK 112
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 571 -----VCRNDQGGPRKMC--LWYVR-----VLCCETPKGCPVYSTS 606
OY 113 GLMSYRIITDPFSLTRNLPQELPOEDSLHGFQSO-----AVPLAHNHTDY 160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 607 VTAESPVLGEPPAQDTQSSWQKSRITTLVYSSITSTQSTASPTTSTTPAIPSTTS 666
OY 161 SKPTDISWRDTLSQKFGSSDHLKLFKMDASAOQLAYKKGHSSQSSQFSDDEIAHL 220
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 667 APTTSTASPTTS-----TTSAPTSTSTSPQTTSAPTSTSTASPTTSAPT 710
OY 221 ENVGSLPRTVAVASP--HTSATPKPATLPTNASVTP-----SGTSQQLATTA 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 711 STISA-PTTSTISAPTSTTSSAPTSTASPTSTSSAPTNTTSTAPTSTTSAITSTIS 769
OY 269 PPTVTVSQPPTTISTVFTAAATLOAMATTAVLTTPQAPDTSKSLJETTFTEISNL 328
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 770 APTTSTSTPQSTTSSPTTSTPTPQSTTSSPTTSTTSTASPTTSTTSTSTPQT 829
```

QY 329 TLNTGVNVNPT-ALSNVSESTMNKTASWEGREASPGSSSGSVPE 374
 DB 830 SSSAPTSSTTSAPTSTISAPTSTSTSTSTSTSTSTSTSTSTSTST 876

RESULT 13

ID Q7YTR7 PRELIMINARY; PRT; 519 AA.
 AC Q7YTR7;
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Hypothetical protein C30H6.11.
 GN C30H6.11.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Felodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Mortimore B.J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81044; CAB17706.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 519 AA; 56012 MW; 93C2CF9EC39D1A CRC64;

Query Match 7.6%; Score 168; DB 5; Length 519;
 Best Local Similarity 27.1%; Pred. No. 0.00023;
 Matches 58; Conservative 22; Mismatches 96; Indels 38; Gaps 7;

QY 229 TVAVASPHNTSATPKATLTPNASTVPSGTSOPQLATTAPVTTYSOPPTTLISTVTT 288
 DB 155 TTTTTPPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTT 214
 QY 289 RAAATLQAMATVAVLTTFQAPTDKSLPTFEISNLTLNTGVNVNPTLMSNVBS 348
 DB 215 TTPPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTT 269
 QY 349 -----STMNKTASWEGREASPGSSSGSVPE-----QYGLPFE---KWLIGSL----- 390
 DB 270 AVNYNYNTDNMAYD-----NNSNNHNSSENFMRMLSLPLAFSINFTLMSIYIQHMK 323
 QY 391 --LFGVLFLVITGLVGLRLSLSELRKRYSLDY 422
 DB 324 YDLTSLFNLGLVTTL-----LMKKIFCNIOY 350

RESULT 14

ID Q14887 PRELIMINARY; PRT; 477 AA.
 AC Q14887;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Mucin (Fragment).
 GN MUC5AC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tracheobronchial mucosa;
 RA Guyonnet-Duperrat V., Audie J., Debailleul V., Laine A., Buisine M.,

RA Zoultina-Gallieue S., Pigny P., Aubert J., Porchet N.;
 RT "Characterization of the human mucin gene MUC5AC: a consensus
 RT cysteine-rich domain for 11p15 mucin genes."
 RL Biochem. J. 0:0-0(1994).
 DR EMBL; Z34277; CAAB4031.1; -.
 DR PIR; S53362; S53362.
 FT NON_TER 477 477 1
 FT NON_TER 477 477 1
 SQ SEQUENCE 477 AA; 50666 MW; E7360031BA51311 CRC64;

Query Match 7.3%; Score 160.5; DB 4; Length 477;
 Best Local Similarity 24.4%; Pred. No. 0.00075;
 Matches 66; Conservative 42; Mismatches 114; Indels 49; Gaps 9;

QY 147 SQAVTPLAHHTDYKSPDISW-----RDTLISQKFGSSDHL-----EKLFXKD----- 189
 DB 15 SQPVTRDCLRCTWTKMFVDPSPGPHGDKETNNIIRSEKICRPEETRLQCRAE 74
 QY 190 ---EASQQLAY-----KEKG-----HSQSQFS--DOEIAHLPEVNSALPATVAVAS 234
 DB 75 SHPEVSIHLGQVQCSREGLVCRNODQGFKMCINYEAVLCCETPKGCPVT---ST 131
 QY 235 PHTSATPKPATLPTLPTNS-----VTPSGTSOPQLATTAPVTTYSOPPTTLI 283
 DB 132 PVTAPSTPSGRATSPGTSWQKSRITTLVTTSTSTSPQTSAPTSTSTSTSTSTST 191
 QY 284 STVFTRAAATLQAMATVAVLTTFQAPTDKSLPTFEISNLTLNTGVNVNPTA 340
 DB 192 SAPTSTSTPQTSISSAPTSSTTSAPTSTSTSTSTSTSTSTSTSTSTSTSTST 251
 QY 341 LMSNVSESTMNKTASWEGREASPGSSSGS 371
 DB 252 TSTTSAPTSTSTSTPQTSKTSAPTSTSTSGS 282

RESULT 15

ID Q8WM05 PRELIMINARY; PRT; 2448 AA.
 AC Q8WM05;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Mucin 5 (Fragment).
 GN MUC5AC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Trachea;
 RX MEDLINE=21426417; PubMed=11535137;
 RT Escande F., Aubert J.P., Porchet N., Buisine M.P.;
 RT "Human mucin gene MUC5AC: organization of its 5'-region and central
 RT repetitive region."
 RL Biochem. J. 358:763-772(2001).
 DR EMBL; AJ296317; CAC83674.1; -.
 DR Genew; HGNC:7515; MUC5AC.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR001209; Ribosomal_S14.
 DR InterPro; IPR002919; TIL_Cyrich.
 DR InterPro; IPR001007; VWF_C.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF01826; TIL; 2.
 DR Pfam; PF00094; vwd; 3.
 DR SMART; SM00214; WVC; 3.
 DR SMART; SM00216; VMD; 3.
 DR PROSITE; PS00527; RIBOSOMAL_S14; 2.
 FT NON_TER 2448 2448
 SQ SEQUENCE 2448 AA; 260970 MW; A5C1BD627844D952 CRC64;

